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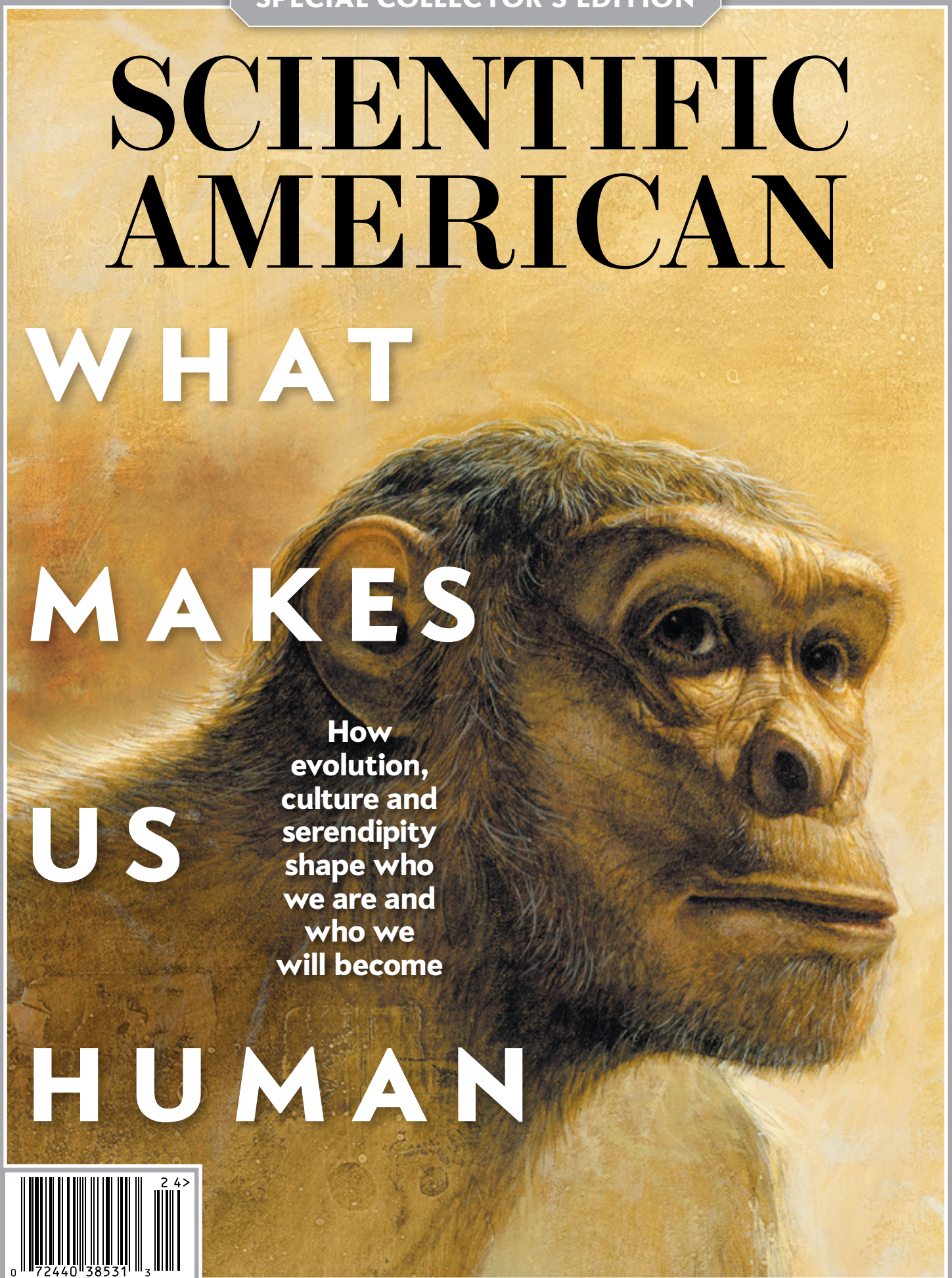
# SCIENTIFIC AMERICAN

# WHAT MAKES US HUMAN

How evolution, culture and serendipity shape who we are and who we will become



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ON THE COVER

This artist's conception is based on seven-million-year-old fossils found in the Djurab Desert of northern Chad and reported in 2002. Nicknamed Toumaï ( "hope of life" in the local Goran language), *Sahelanthropus tchadensis* is the oldest putative member of the human lineage, having lived several million years before "Lucy" and the other australopithecines. Painting by Kazuhiko Sano.

SCIENTIFIC AMERICAN

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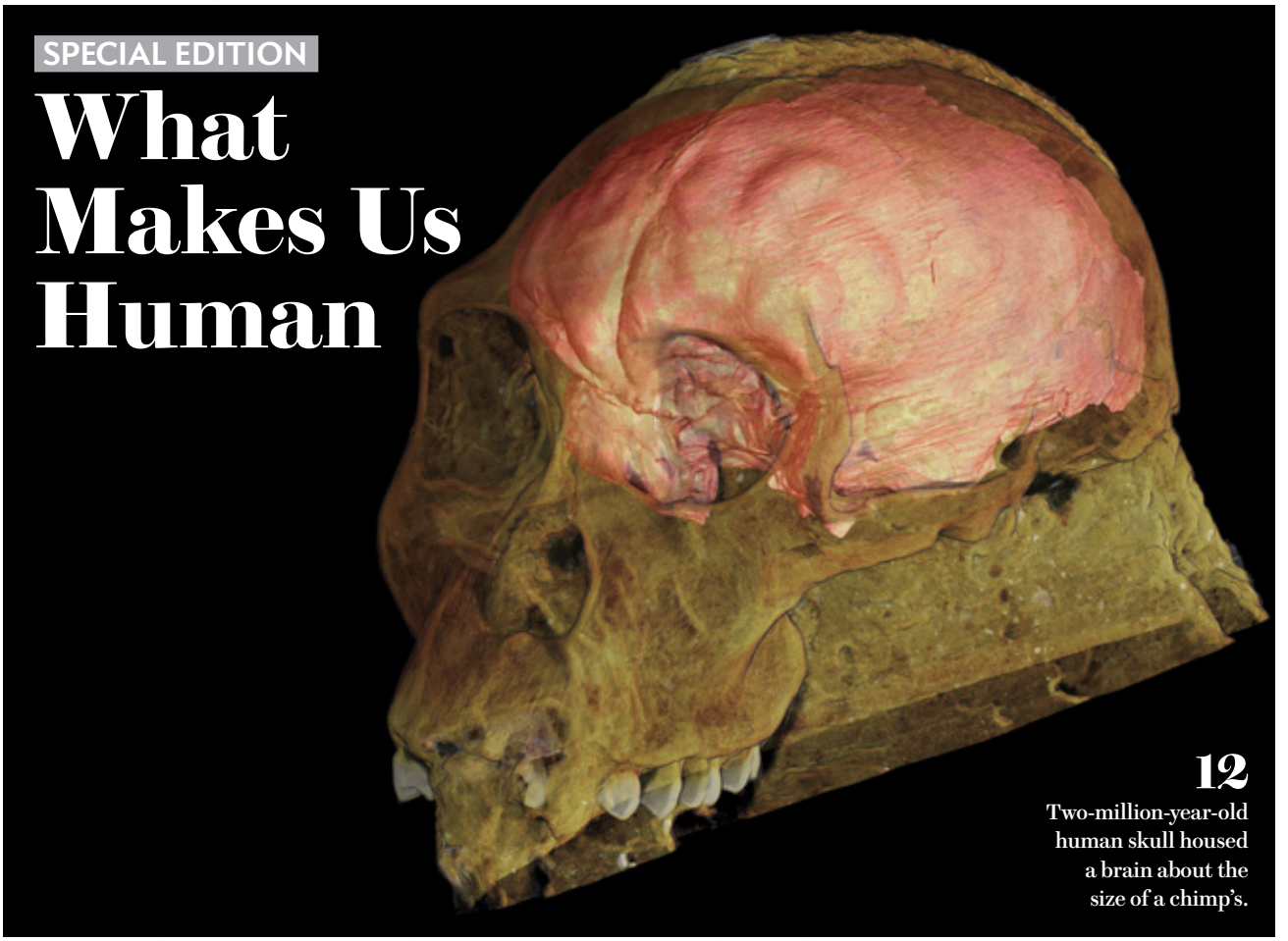
SPECIAL EDITION

# What Makes Us Human



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Articles in this special issue are updated from previous issues of *Scientific American*.


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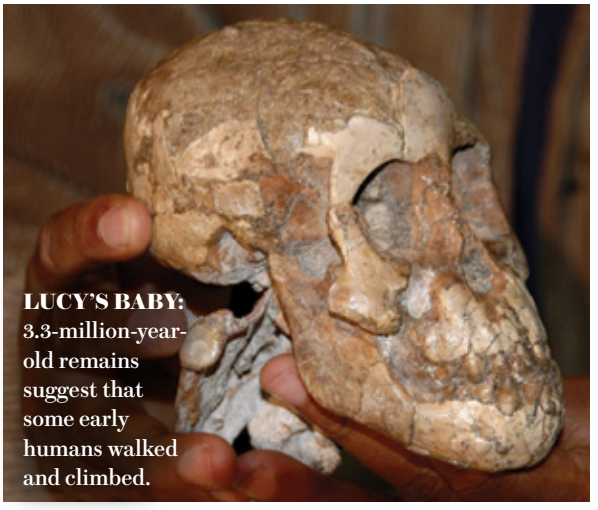
# The Sprawling Story of Human Evolution

WE HUMANS ARE A STRANGE bunch. We have self-awareness and yet often act on impulses that remain hidden. We were forged in adversity but live in a world of plenty. Who are we? What is to become of us? To these age-old questions, science has in recent years brought powerful tools and reams of data.

We know, for instance, that three million years ago, a group of primates known as the australopithecines was walking capably on two legs—the better to navigate the African savanna—and yet still had long arms suited to life in the trees. In searching for clues to what selective pressures drove this transition, paleontologists discovered a 3.3-million-year-old fossil—"Lucy's baby"—confirming that the famous *Australopithecus afarensis* skeleton "Lucy" indeed contains a mosaic of traits related to both walking and climbing (*page 4*). Other paleontologists have uncovered remains of a previously unknown human species in South Africa (*page 12*).



**LUCY'S BABY:** 3.3-million-year-old remains suggest that some early humans walked and climbed.

EUAN DENHOLM *Reuters*; SCIENTIFIC AMERICAN IS A TRADEMARK OF SCIENTIFIC AMERICAN, INC., USED WITH PERMISSION

Once we came down out of the trees, we lost our hair. Why? It may sound like a dumb question from the back of the classroom, but scientists have asked it and found that a lack of body hair was essential for keeping our primeval bodies cool (*page 22*).

Genetics opens a big window onto our human ancestry. If we share nearly 99 percent of our DNA with chimps, why are we, not them, living in the suburbs and driving cars? How does a small amount of DNA make such a big difference? To find out, biostatistician Katherine S. Pollard and others are figuring out what that 1 percent of DNA is and what it does—her account is in this issue (*page 30*). We also look at how scientists are studying the minuscule bits of DNA that differ from one individual to another for clues to our origins and evolution (*page 60*).

Human evolution and culture are often intertwined. For instance, as humans started to live longer, grandparents played a role in family life, which in turn made possible more complex social behaviors (*page 38*).

The more we learn about our own evolution, the more complicated the story becomes. New findings have pushed back the date at which hunter-gatherers colonized the Americas (*page 68*). And the discovery of "hobbits"—a human species of small stature—has turned the science of human origins on its ear (*page 84*).

Where is evolution taking us? We present two points of view. Jonathan K. Pritchard, professor of human genetics at the University of Chicago, argues that selection pressure typically acts over tens of thousands of years (*page 98*), which means we probably won't evolve much anytime soon. But stasis is only one possible future, says University of Washington astrobiologist Peter Ward. In adapting to new environments—say, a colony on Mars—our human species may eventually diverge into two or more. Or we could go the cyborg route and merge with machines (*page 106*). Whichever option you prefer, there is plenty to ponder. SA

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**BABY FACE:** The skeleton of a juvenile *Australopithecus afarensis* nicknamed Selam is more complete than even the well-known Lucy fossil. And whereas much of Lucy's face is missing, Selam's is exquisitely preserved.



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An earlier version of this story was posted on www.ScientificAmerican.com. Readers were invited to send in their comments and questions, and scientists were asked to provide commentaries. That feedback helped to shape the article that follows.

# LUCY'S BABY

## An ancient infant skeleton yields new insight into how humans evolved to walk upright

**BY KATE WONG**

THE ARID BADLANDS OF ETHIOPIA'S REMOTE AFAR REGION HAVE LONG BEEN A FAVORITE hunting ground for paleoanthropologists. Many hominins—the group that includes all the creatures in the human line since it branched away from that of the chimps—once called it home. The area is perhaps best known for having yielded "Lucy," the 3.2-million-year-old skeleton of a human ancestor known as *Australopithecus afarensis*. In 2006 researchers unveiled another incredible *A. afarensis* specimen from a site called Dikika, just four kilometers from where Lucy turned up. But unlike Lucy, who was well into adulthood by the time she died, the recently discovered fossil is that of an infant, one who lived 3.3 million years ago (and yet has nonetheless been dubbed "Lucy's baby").

**IN BRIEF**

**Researchers** working in northeastern Ethiopia found the remains of a baby *Australopithecus afarensis,* a species believed to be ancestral to our own. **Some 3.3 million years old,** the spectacularly complete skeleton is the earliest child in the human fossil record. **Preserving bones** never before known for *A. afarensis,* the specimen is raising questions about how our ancestors became bipedal. **The Dikika infant** may also illuminate the order in which other body parts changed over the course of human evolution.

EUAN DENHOLM *Reuters*



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No other hominin skeleton of such antiquity—including Lucy—is as complete as this one. Moreover, as the earliest juvenile hominin ever found, the Dikika child provides an unprecedented opportunity to study growth processes in our ancient relatives. "If Lucy was the greatest fossil discovery of the 20th century," says Donald C. Johanson of Arizona State University, who unearthed the famed fossil in 1974, "then this baby is the greatest find of the 21st thus far."

### BUNDLE OF JOY

IT WAS THE AFTERNOON of December 10, 2000, when fossil hunters led by Zeresenay Alemseged, now at the California Academy of Sciences in San Francisco, spotted the specimen. Only part of its tiny face was visible; most of the rest of the skeleton was entombed in a melon-size block of sandstone. But "right away it was clear it was a hominin," Alemseged recollects, noting the smoothness of the brow and the small size of the canine teeth, among other humanlike characteristics. Further evaluation, however, would have to wait until the fossil was cleaned—a painstaking process in which the cementlike matrix is removed from the bone almost grain by grain with dental tools.

It took Alemseged five years to expose key elements of the child's anatomy; he continues to analyze bones revealed since then. Still, the find has already surrendered precious insights into a species that most researchers believe gave rise to our own genus, *Homo*. Alemseged and his colleagues described the fossil and its geologic and paleontological context in two papers published in 2006 in *Nature*. And at a press conference held in Ethiopia to announce the discovery, they christened the child Selam—"peace" in several Ethiopian languages—in hopes of encouraging harmony among the warring tribes of Afar.

**"You don't just magically flip some evolutionary switch somewhere and transmute a quadruped into an upright-walking bipedal human."**
**—Donald C. Johanson**

The skeleton, judged to be that of a three-year-old girl, consists of a virtually complete skull, the entire torso, and parts of the arms and legs. Even the kneecaps—which are no larger than macadamia nuts—are preserved. Many of the bones are still in articulation. Hominin fossils this complete are incredibly rare, and ones of infants are rarer still because their bones are that much more fragile. Indeed, the next oldest skeleton of a juvenile that is comparably intact is a Neandertal baby dating to around 50,000 years ago.

### WALKING VS. CLIMBING

THE EXCEPTIONAL PRESERVATION of Selam, as well as that of other animals found at the site, indicates to team geologist Jonathan G. Wynn of the University of South Florida that her body was buried shortly after death by a flood event. Whether she perished in the flood or before it is unknown.

Although she was only three when she died, Selam already possessed the distinctive characteristics of her species. Her projecting snout and narrow nasal bones, for example, readily distinguish her from another ancient youngster, the so-called Taung child from South Africa, who was a member of the closely related *Australopithecus africanus* species. And her lower jaw resembles mandibles from Hadar, the site where Lucy and a number of other *A. afarensis* individuals were found.

Selam also exhibits the same mash-up of traits in her postcra-

COURTESY OF DENNÉ REED *University of Texas at Austin (left)*; COURTESY OF JONATHAN G. WYNN *University of South Florida (right)*



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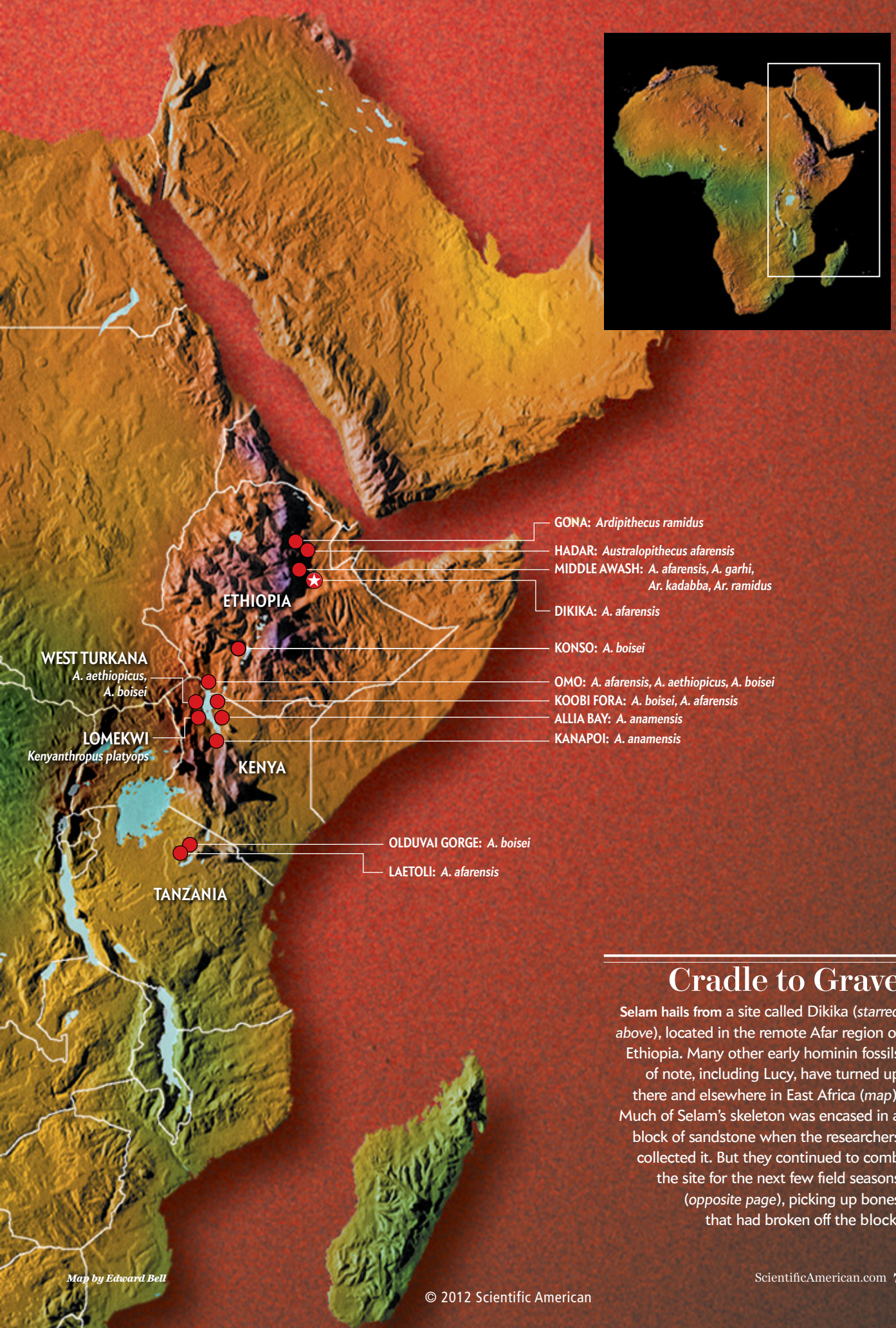


*Map by Edward Bell*

# Cradle to Grave

**Selam hails from** a site called Dikika (*starred above*), located in the remote Afar region of Ethiopia. Many other early hominin fossils of note, including Lucy, have turned up there and elsewhere in East Africa (*map*). Much of Selam's skeleton was encased in a block of sandstone when the researchers collected it. But they continued to comb the site for the next few field seasons (*opposite page*), picking up bones that had broken off the block.

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# Spectacular Skeleton

**Selam is one** of the most complete early hominin skeletons ever found, although many of the bones are still at least partially obscured by sandstone. In the drawing below, based on an adult *A. afarensis,* the bones believed to be present in the specimen in 2006 are shaded in gold.

Features of Selam's face, including the small, narrow nasal bones (*a*), identify her as *A. afarensis,* as opposed to the closely related *A. africanus*. Although much of the braincase is missing, the fossil preserves a natural sandstone endocast, or impression of the interior of the skull (*b*). The apparent brain size hints that *A. afarensis* may have had delayed brain growth relative to chimps, which is a characteristic of modern humans.

Computed tomography revealed that in addition to having a full set of milk teeth, the child had permanent teeth waiting to come in (*c*). The remains also include a delicate bone known as the hyoid (*d*), which helps to anchor the tongue and the voice box. It is only the second hominin hyoid ever found—the first came from a 60,000-year-old Neandertal skeleton. Its morphology suggests that *A. afarensis* had a chimplike voice box.

Like other *A. afarensis* individuals, Selam has a number of traits in her leg bones (*e*) and foot bones (*f*) that indicate she walked bipedally on the ground. Her heel, for example, exhibits a humanlike wideness. But her upper body seems partly adapted for life in the trees. She has long, curved fingers (*g*) that would have aided in grasping tree branches. And the socket of her shoulder blade, or scapula (*h*), faces upward like an ape's, rather than to the side like a human's.

The scapula is a bone of contention, however. According to the discoverers, it looks most like that of a gorilla. But critics charge that the bone is actually rather humanlike, particularly in the relative proportions of the depressed areas for muscle attachment on either side of the ridge that divides the blade.

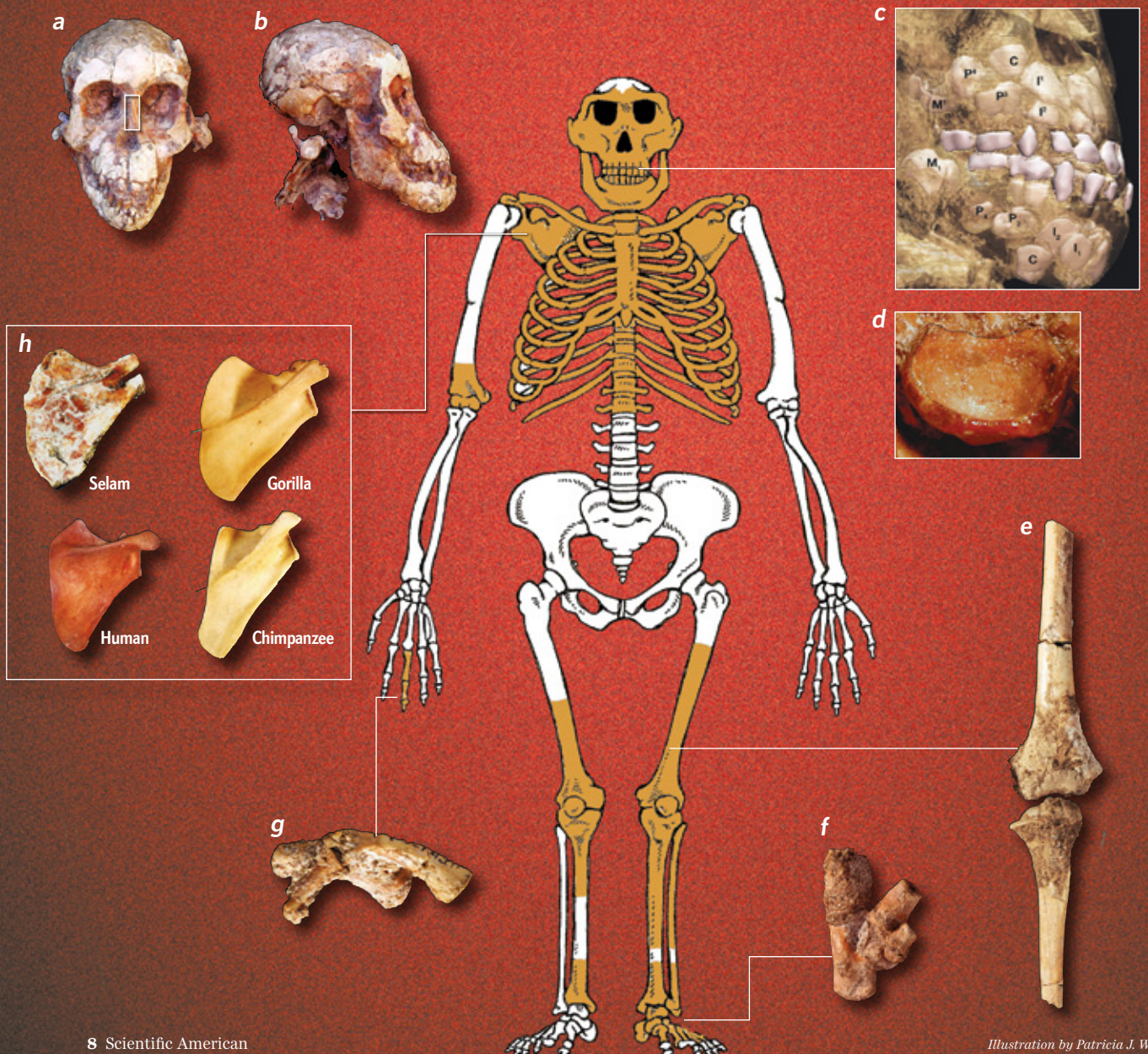


*Illustration by Patricia J. Wynne*



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nial skeleton that has long irked scientists interested in how *A. afarensis* moved around the landscape. Scholars agree that *A. afarensis* was a creature that got around capably on two legs. But starting in the 1980s, a debate erupted over whether the species was also adapted for life in the trees. The argument centered on the observation that whereas the species has clear adaptations to bipedal walking in its lower body, its upper body contains a number of primitive traits better suited to an arboreal existence, such as long, curved fingers for grasping tree branches. One camp held that *A. afarensis* had made a full transition to terrestrial life and that the tree-friendly features of the upper body were just evolutionary baggage handed down from an arboreal ancestor. The other side contended that if *A. afarensis* had retained those traits for hundreds of thousands of years, then tree climbing must have still formed an important part of its locomotor repertoire.

Like her conspecifics, Selam has legs built for walking and fingers built for climbing. But she also brings new data to the controversy in the form of two shoulder blades, or scapulae—bones previously unknown for this species. According to Alemseged, her scapulae look most like those of a gorilla. The upward-facing shoulder socket is particularly apelike, contrasting sharply with the laterally facing socket modern humans have. This orientation, Alemseged points out, may have facilitated raising the hands above the head—something primates do when they climb. (Although gorillas do not climb as adults, they do spend time in the trees as youngsters.)

**TEAM LED BY** Ethiopian paleoanthropologist Zeresenay Alemseged found Selam's remains.

Further hints of arboreal tendencies reside in the baby's inner ear. Using computed tomographic imaging, the team was able to glimpse her semicircular canal system, which is important for maintaining balance. The researchers determined that Selam's semicircular canals are similar to those of African apes and *A. africanus*. This, they suggest, could indicate that *A. afarensis* was not as fast and agile on two legs as we modern humans are. It could also mean that *A. afarensis* was limited in its ability to decouple the movements of its head and torso, a feat that seems to play a key role in endurance running in our own species.

# What Readers Wanted to Know

In an earlier version of this article, posted on our Web site, we invited readers to submit any questions they had about Selam. Kate Wong answered their questions in the blog. An edited selection of those exchanges follows.

***How was Selam's age at death assessed?*** **—Stephen**

***A:*** Selam's age was estimated based on her apparent stage of dental development. Using comparable data from African apes, the researchers judged her to be about three years old when she died. But *Australopithecus afarensis* no doubt had a developmental schedule that differed from that of chimps and gorillas, so this is only an educated guess.

***How was sex determined?*** **—Debra Martin**

***A:*** The skeleton is believed to be that of a female based on computed tomographic measurements of the fully formed permanent tooth crowns still embedded in the jaws. When compared with measurements of teeth from *A. afarensis* individuals from the sites of Hadar, Laetoli and Maka, the Dikika child's teeth grouped closely with those of confirmed females.

***What is the uncertainty of the measurement of the age of a fossil like Selam? What technology is used?*** **—Juan Moreira**

***A:*** Diana C. Roman of the University of South Florida dated the fossil by ascertaining the ages of the layers of volcanic ash around Selam. One layer was deposited before the child died; the other was deposited some time after she died. By interpolating the position of the fossil relative to those two layers, Roman determined that the fossil was between 3.31 million and 3.35 million years old—an uncertainty of 40,000 years.

***What's the big deal? We know that our ancestors had to come down out of the trees sometime. Kids nowadays have a predilection for climbing trees, too. (Maybe an unconscious link to an arboreal past?)*** **—Matthew T.**

***A:*** The question is to what extent *A. afarensis* was adapted for terrestriality. No one is suggesting that *A. afarensis* could not get up into a tree under any circumstances—as you correctly point out, humans can still do that—the debate is over whether it was adapted to do so. It's a big deal because bipedalism is a hallmark of human evolution, so paleoanthropologists are eager to understand the details of how it emerged.

***Are there any plant or animal fossils associated with* A. afarensis *finds that would indicate what kind of environment they lived in?*** **—Traveler**

***A:*** The animal fossils found at Dikika indicate that the child inhabited a moist, mosaic environment composed of woodlands and grasslands, with permanent water nearby. This is very similar to the environment in which Lucy and other representatives of *A. afarensis* lived.

***What does the animal have to gain from being able to engage in endurance running?*** **—Donald McMiken**

***A:*** Endurance running has been hypothesized to have given early humans a leg up (if you will) in hunting or scavenging, by allowing them to wear the prey out or reach the carcass faster, respectively.

FROM "A JUVENILE EARLY HOMININ SKELETON FROM DIKIKA, ETHIOPIA," BY ZERESENAY ALEMSEGED ET AL., IN *NATURE*, VOL. 443, SEPTEMBER 21, 2006 (*opposite page, all bones*); COURTESY OF DENNÉ REED *University of Texas at Austin (Alemseged)*



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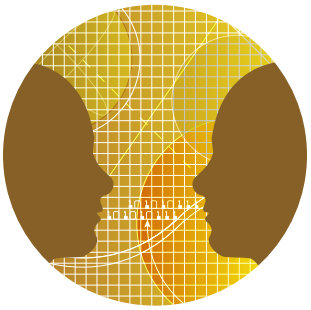
## What the Experts Said

We polled the experts for their thoughts on the discovery of Selam shortly after the find was announced. Their views are encapsulated here.



**John Hawks of the University of Wisconsin–Madison** wondered whether Selam spells the end of a hotly contested hominin genus. In 2001 paleoanthropologists announced that they had found a fairly complete skull and some jaws and teeth at a site called Lomekwi in Kenya. They assigned the 3.5-million-year-old remains to a new genus of hominin, *Kenyanthropus.* Skeptics counter that the fossils are instead a regional variant of *A. afarensis.* It is an obvious sample with which to compare Selam. But oddly enough, no mention of *Kenyanthropus* appears in the formal description of the child.

**Ralph L. Holloway of Columbia University** hoped that the brain endocast would show enough details in the so-called Broca's regions and the occipital region to reveal a posterior placement of the lunate sulcus, a curved depression in the brain's surface. This would indicate a definite reorganizational pattern of the cerebral cortex toward a more humanlike rather than chimplike or gorillalike pattern.

**C. Owen Lovejoy of Kent State University** made the case that rather than reopening the debate over whether *A. afarensis* was a dedicated biped or whether it also spent some time in the trees, the Dikika child firmly closes it in favor of the species being strictly bipedal. Although the shoulder blade bears some resemblances to the gorilla shoulder blade, it actually shows some striking similarities with the human shoulder blade.

Also, the fact that the youngster already had curved fingers at age three suggests that this is an inherited, primitive characteristic—as opposed to the individual having developed curved fingers as a result of grasping tree branches, which is what the arborealists envision.

**René Bobe of George Washington University** observed that one of the many important aspects of this fossil is that its geologic and paleontological context can be studied in detail. Dikika reveals hominin adaptations and environments that existed just before major climatic changes led to the ice ages, before *Homo* made its first appearance in the fossil record and before the earliest known stone tools. In Selam's day, Dikika was largely a lush, forested place. But by the time *Homo erectus* emerged, a little less than two million years ago, grasslands were much more prominent.

**William E. H. Harcourt-Smith of the American Museum of Natural History** in New York City argued that features of Selam's upper limbs and inner ear are strong evidence that *A. afarensis* was partly arboreal. It will be very interesting, he said, to see whether analyses of her foot reveal that she was able to move her big toe so as to grasp branches. In his view, the first obligate bipeds were early members of our own genus, *Homo.*

The conclusion that *A. afarensis* was a bipedal creature with an upper body at least partly adapted for life in the trees echoes what Jack T. Stern, Jr., of Stony Brook University and his colleagues wrote years ago in their reports on Lucy and her contemporaries. "I was happy to see that this paper suggests I might have been right," Stern comments. Johanson agrees that the case for a partly arboreal *A. afarensis* is stronger than it once was. "Early on I was a staunch advocate of strict terrestrial bipedalism in *afarensis*," he remarks. But taking more recent findings into consideration, Johanson says, "it's not out of the realm of possibility that they were still exploiting some of the arboreal habitats for getting off the ground at night and sleeping up there or going back to familiar food sources."

A combination of walking and climbing would fit neatly with the picture that is emerging from studies of the environments of early hominins, including Selam. Today Dikika is an expanse of dusty hills dotted with only the occasional tree or shrub. But 3.3 million years ago, it was a well-watered delta flanked by forests, with some grasslands nearby. "In this context, it is not surprising to have an 'ape' that spends time in the trees and on the ground," comments project member René Bobe, now at George Washington University.

Not everyone is persuaded by the arboreal argument. C. Owen Lovejoy of Kent State University disputes the claim that Selam's scapula looks like a gorilla's. "It's primitive, but it's really more humanlike than gorillalike," he remarks. Lovejoy, a leading proponent of the idea that *A. afarensis* was a dedicated biped, maintains that the forelimb features that are typically held up as indicators that *A. afarensis* spent time in the trees

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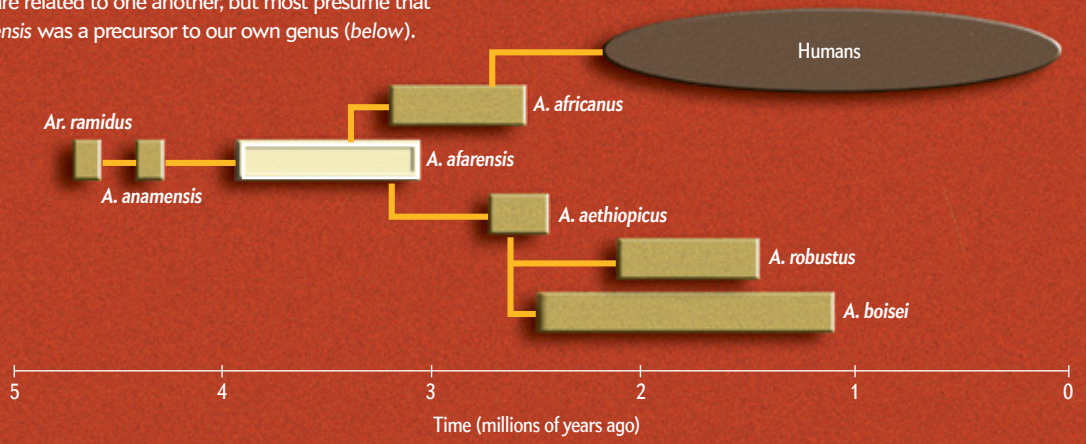
## An Ancient Ancestor

***A. afarensis*** is but one of many australopithecine species known to science [*see reconstruction at bottom on opposite page*]. Researchers disagree about exactly how these species are related to one another, but most presume that *A. afarensis* was a precursor to our own genus (*below*).




only provide "evidence that the animal has an arboreal history." The discovery of the famed Laetoli footprints in 1978 closed the debate, he states. The trail did not show a prehensile big toe, without which, Lovejoy says, *A. afarensis* simply could not move about effectively in the trees.

### A HODGEPODGE HOMININ

EXPERTS MAY DISAGREE over the functional significance of Selam's apelike skeletal characteristics, but they concur that different parts of the hominin body were undergoing selection at different times. *A. afarensis* is "a good example of mosaic evolution," Johanson states. "You don't just magically flip some evolutionary switch somewhere and transmute a quadruped into an upright-walking bipedal human." It looks like natural selection is selecting for bipedalism in the lower limbs and pelvis first, and things that are not really used in bipedal locomotion, such as arms and shoulders, change at a later stage, he says. "We're getting to know more and more about the sequence of changes" that produced a terrestrial biped from a tree-dwelling, apelike creature.

Analysis of Selam's skull hints at a similarly piecemeal metamorphosis. The shape of the hyoid—a delicate, rarely preserved bone that helps to anchor the tongue and the voice box—indicates that *A. afarensis* had air sacs in its throat, suggesting the species possessed an apelike voice box. Conversely, the child's brain shows a subtle sign of humanity. By studying the fossil's natural sandstone endocast, an impression of the braincase, Alemseged's team ascertained that Selam had attained only 65 to 88 percent of the adult brain size by the age of three. A chimp of comparable age, in contrast, has reached more than 90 percent of its adult brain size. This raises the tantalizing possibility that *A. afarensis* experienced a more humanlike pattern of brain growth.

More fossils are needed to discern whether the new skeleton is representative of *A. afarensis* infants, and scientists are doubtless eager to recover remains of other *A. afarensis* children of different ages—if they ever can—to see how they compare. But the little girl from Dikika still has more secrets to spill. "I think the impact of this specimen will be in its information of the growth and development of *Australopithecus,* not only for individual body parts but for rates of development among structures within one individual," observes Carol V. Ward of the University of Missouri–Columbia.

Since the initial description of Selam, continued removal of the sandstone adhering to her remains has exposed all of the bones to some extent. Alemseged expects that he will eventually be able to reconstruct nearly the entire body of an *A. afarensis* three-year-old—and begin to understand what growing up australopithecine was all about. SA

**KATE WONG** is a senior editor at *Scientific American*.

MORE TO EXPLORE

**New Look at Human Evolution.** Special edition. *Scientific American,* Vol. 13, No. 2; 2003.
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**A Juvenile Early Hominin Skeleton from Dikika, Ethiopia.** Zeresenay Alemseged et al. in *Nature,* Vol. 443, pages 296–301; September 21, 2006.
**From Lucy to Language.** Donald Johanson and Blake Edgar. Simon & Schuster, 2006.
**Lucy's Legacy: The Quest for Human Origins.** Donald C. Johanson and Kate Wong. Broadway, 2010.
Extended coverage of Lucy's baby—including more interviews, commentaries and photographs—can be found at **www.ScientificAmerican.com/article.cfm?id=special-report-lucys-baby**

COURTESY OF AMERICAN MUSEUM OF NATURAL HISTORY, NEW YORK (*opposite page: reconstruction*); MELISSA THOMAS (*timeline*)



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PALEOANTHROPOLOGY

# First of Our Kind

Sensational fossils from South Africa spark a debate over the origins of *Homo*

BY KATE WONG

SOMETIME BETWEEN THREE MILLION AND TWO MILLION years ago, perhaps on a primeval savanna in Africa, our ancestors became recognizably human. For more than a million years their australopithecine predecessors—Lucy and her kind, who walked upright like us yet still possessed the stubby legs, tree-climbing hands and small brains of their ape forebearers—had thrived in and around the continent's forests and woodlands. But their world was changing. Shifting climate favored the spread of open grasslands, and the early australopithecines gave rise to new lineages. One of these offshoots evolved long legs, toolmaking hands and an enormous brain. This was our genus, *Homo,* the primate that would rule the planet.

For decades paleoanthropologists have combed remote corners of Africa on hand and knee for fossils of *Homo*'s earliest representatives, seeking to understand the details of how our genus rose to prominence. Their efforts have brought only modest gains—a jawbone here, a handful of teeth there. Most of the recovered fossils instead belong to either ancestral australopithecines or later members of *Homo*—creatures too advanced to illuminate the order in which our distinctive traits arose or the selective pressures that fostered their emergence. Specimens older than two million years with multiple skeletal elements preserved that could reveal how the *Homo* body plan came to-

IN BRIEF

**The origin of our genus,** *Homo,* is one of the biggest mysteries facing scholars of human evolution. **Based on the meager evidence** available, scientists have surmised that *Homo* arose in East Africa, with Lucy's species, *Australopithecus afarensis,* giving rise to the founding member of our lineage, *Homo habilis.* Now fossils from a site northwest of Johannesburg, South Africa, could upend that scenario. **The fossils represent** a previously unknown species of human with an amalgam of australopithecine and *Homo* traits that suggest to its discoverers that it could be the ancestor of *Homo.*

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**NEW HUMAN SPECIES** from South Africa—*Australopithecus sediba*—has been held up as the ancestor of our genus, *Homo*.

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gether eluded discovery. Scientists' best guess is that the transition occurred in East Africa, where the oldest fossils attributed to *Homo* have turned up, and that *Homo*'s hallmark characteristics allowed it to incorporate more meat into its diet—a rich source of calories in an environment where fruits and nuts had become scarce. But with so little evidence to go on, the origin of our genus has remained as mysterious as ever.

Lee Berger thinks he has found a big piece of the puzzle. A paleoanthropologist at the University of the Witwatersrand in Johannesburg, South Africa, he recently discovered a trove of fossils that he and his team believe could revolutionize researchers' understanding of *Homo*'s roots. In the white-walled confines of room 210 at the university's Institute for Human Evolution, he watches as Bernard Wood of George Washington University paces in front of the four plastic cases that have been removed from their fireproof safe and placed on a table clothed in royal blue velvet. The foam-lined cases are open, revealing the nearly two-million-year-old fossils inside. One holds pelvis and leg bones. Another contains ribs and vertebrae. A third displays arm bones and a clavicle. And a fourth houses a skull. On a counter opposite the table, more cases hold a second partial skeleton, including a nearly complete hand.

Wood, a highly influential figure in the field, pauses in front of the skull and leans in for a closer look. He strokes his beard as he considers the dainty teeth, the grapefruit-size braincase. Straightening back up, he shakes his head. "I'm not often at a loss for words," he says slowly, "but wow. Just wow."

Berger grins. He has seen this reaction before. Since he unveiled the finds in 2010, scientists from all over the world have been flocking to his lab to gawk at the breathtaking fossils. Based on the unique anatomical package the skeletons present, Berger and his team assigned the remains to a new species, *Australopithecus sediba*. They furthermore propose that the combination of primitive *Australopithecus* traits and advanced *Homo* traits evident in the bones qualifies the species for a privileged place on the family tree: as the ancestor of *Homo*. The stakes are high. If Berger is right, paleoanthropologists will have to completely rethink where, when and how *Homo* got its start—and what it means to be human in the first place.

## THE ROAD NOT TAKEN

IN THE MIDDLE of the rock-strewn dirt road that winds through the John Nash Nature Reserve, Berger brings the Jeep to a halt and points to a smaller road that branches right. For 17 years he had made the 40-kilometer trip northwest from Johannesburg to the 9,000-hectare parcel of privately owned wilderness and driven past this turnoff, continuing along the main road, past the resident giraffes and warthogs and wildebeests, to a cave he was excavating just a few kilometers away called Gladysvale. In 1948 American paleontologists Frank Peabody and Charles Camp came to this area to look for fossils of hominins (modern humans and their extinct relatives) on the advice of famed South African paleontologist Robert Broom, who had found such fossils in the caves of Sterkfontein and Swartkrans, eight kilometers away. Peabody suspected that Broom had intentionally sent them on a wild goose chase, so unimpressed was he with the sites here. Little did Berger or the expeditioners before him know that had they only followed this smaller path—one of several miners' tracks used in the early 1900s to

1

2

**LEE BERGER** (*left*) and Meshack Kgasi (*right*) inspect the miners' pit at the Malapa site, where Berger discovered *A. sediba* (*1*). Blocks of concretelike calcified clastic sediment dislodged by miners will be CT-scanned to see if they contain fossils (*2*). View captures the valleys in and around the Malapa area, northwest of Johannesburg in South Africa (*3*).



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cart the limestone that built Johannesburg from quarries out to the main road—they would have made the discovery of a lifetime.

Berger, now 46 years old, never imagined he would find something like *A. sediba*. Although he thought *Homo* might have had roots in South Africa instead of East Africa, he knew the odds of making a big find were slim. Hominin fossils are extremely rare, so "you don't have any expectations," he reflects. What is more, he was focused on the so-called Cradle of Humankind, an already intensively explored region whose caves had long been yielding australopithecines generally considered to be more distantly related to *Homo* than the East African australopithecines seemed to be. And so Berger continued to toil at Gladysvale day after day, year after year. Because he found little in the way of hominins among the millions of animal fossils there, he busied himself with another goal: dating the site. A critical problem with interpreting the South African hominin fossils was that scientists had not yet figured out how to reliably determine how old they were. In East Africa, hominin fossils come from sediments sandwiched between layers of volcanic ash that blanketed the landscape during long-ago eruptions. Geologists can ascertain how old an ash layer is by analyzing its chemical "fingerprint." A fossil that originates from a layer of sediment that sits in between two volcanic ashes is thus intermediate in age between those two ashes. The cave sites in the Cradle of Humankind lack volcanic ashes, but through his 17 years of trial and error at Gladysvale, Berger and his colleagues hit on techniques that circumvented the problem.

Those techniques would soon come in very handy. On August 1, 2008, while surveying the reserve for potential new fossil sites in the area that he had identified using Google Earth, Berger turned right on the miners' track he had passed by for 17 years and followed it to a three- by four-meter hole in the ground blasted by the miners. Eyeballing the site, he found a handful of animal fossils—enough to warrant a trip back for a closer look. He returned on August 15 with his then nine-year-old son, Matthew, and dog, Tau. Matthew took off into the bush after Tau, and within minutes he shouted to his father that he had found a fossil. Berger doubted it was anything important—probably just an antelope bone—but in a show of fatherly support, he made his way over to inspect the find. There, protruding from a dark hunk of rock nestled in the tall grass by the corpse of a lightning-struck tree, was the tip of a collarbone.

As soon as Berger laid eyes on it, he knew it belonged to a hominin. In the months that followed he found more of the clavicle's owner, along with another partial skeleton, 20 meters away in the miners' pit. To date, Berger and his team have recovered more than 220 bones of *A. sediba* from the site—more than all the known early *Homo* bones combined. He christened the site Malapa, meaning "homestead" in the local



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Sesotho language. Using the approaches honed at Gladysvale, the geologists on Berger's team would later date the remains with remarkable precision to 1.977 million years ago, give or take 2,000 years.

### A PATCHWORK PREDECESSOR

THAT THE MALAPA FOSSILS include so many body parts is important because it means they can offer unique insights into the order in which key *Homo* traits appeared. And what they show very clearly is that quintessentially human features did not necessarily evolve as a package deal, as was thought. Take the pelvis and the brain, for example. Conventional wisdom holds that the broad, flat pelvis of australopithecines evolved into the bowl-shaped pelvis seen in the bigger-brained *Homo* to allow delivery of babies with larger heads. Yet *A. sediba* has a *Homo*-like pelvis with a broad birth canal in conjunction with a teeny brain—just 420 cubic centimeters, a third of the size of our own brain. This combination shows brain expansion was not driving the metamorphosis of the pelvis in *A. sediba*'s lineage.

Not only do the *A. sediba* fossils mingle old and new versions of general features, such as brain size and pelvis shape, but the pattern repeats at deeper levels, like an evolutionary fractal. Analysis of the interior of the young male's braincase shows that the brain, while small, possessed an expanded frontal region, indicating an advanced reorganization of gray matter; the adult female's upper limb pairs a long arm—a primitive holdover from a tree-dwelling ancestor—with short, straight fingers adapted to making and using tools (although the muscle markings on the bones attest to powerful, apelike grasping capabilities). In some instances, the juxtaposition of old and new is so improbable that had the bones not been found joined together, researchers would have interpreted them as belonging to entirely different creatures. The foot, for instance, combines a heel bone like an ancient ape's with an anklebone like *Homo*'s, according to Malapa team member Bernard Zipfel of the University of the Witwatersrand. It is as if evolution was playing Mr. Potato Head, as Berger puts it.

**Had the bones not been found joined together, researchers would have interpreted them as belonging to entirely different creatures.**

The extreme mosaicism evident in *A. sediba,* Berger says, should be a lesson to paleoanthropologists. Had he found any number of its bones in isolation, he would have classified them differently. Based on the pelvis, he could have called it *Homo erectus*. The arm alone suggests an ape. The anklebone is a match for a modern human's. And like the blind men studying the individual parts of the elephant, he would have been wrong. "*Sediba* shows that one can no longer assign isolated bones to a genus," Berger asserts. That means, in his view, finds such as a 2.3-million-year-old upper jaw from Hadar, Ethiopia, that has been held up as the earliest trace of *Homo* cannot safely be assumed to have belonged to the *Homo* line.

Taking that jaw out of the running would make *A. sediba* older than any of the well-dated *Homo* fossils but still younger than *A. afarensis,* putting it in pole position for the immediate ancestor of the genus, Berger's team contends. Furthermore, considering *A. sediba*'s advanced features, the researchers propose that it could be specifically ancestral to *H. erectus* (a portion of which is considered by some to be a different species called *Homo ergaster*). Thus, instead of the traditional view in which *A. afarensis* begat *Homo habilis,* which begat *H. erectus,* he submits that *Australopithecus africanus* is the likely ancestor of *A. sediba,* which spawned *H. erectus.*

If so, that arrangement would relegate *H. habilis* to a dead-end side branch of the human family tree. It might even kick *A. afarensis*—long considered the ancestor of all later hominins, including *A. africanus* and *Homo*—to the evolutionary curb, too. Berger points out that *A. sediba*'s heel is more primitive than that of *A. afarensis,* indicating that *A. sediba* either underwent an evolutionary reversal toward a more primitive heel or that it descended from a different lineage than the one that includes *A. afarensis* and *A. africanus*—one that has yet to be discovered.

"In the South, we have a saying: 'You dance with the girl you brought,'" quips Berger, who grew up on a farm in Sylvania, Ga. "And that is what paleoanthropologists have been doing" in trying to piece together the origin of *Homo* from the fossils that have turned up in East Africa. "Now we have to recognize there is more potential out there," he states. Maybe the East Side story of human origins is wrong. The traditional view of South Africa's oldest hominin fossils is that they represent a separate evolutionary experiment that ultimately fizzled out. *A. sediba* could turn the tables and reveal, in South Africa, another lineage, the one that ultimately gave rise to humankind as we know it (indeed, *sediba* is the Sesotho word for "fountain" or "wellspring").

William Kimbel of Arizona State University, who led the team that found the 2.3-million-year-old jawbone in Ethiopia, is having none of it. The idea that one needs a skeleton to classify a specimen is a "nonsensical argument," he retorts. The key is to find pieces of anatomy that contain diagnostic traits, he says, and the Hadar jaw has features clearly linking it to *Homo,* such as the parabolic shape formed by its tooth rows. Kimbel, who has seen the Malapa fossils but not studied them in depth, finds their *Homo*-like traits intriguing, although he is not sure what to make of them. He scoffs at the suggestion that they are directly ancestral to *H. erectus,* however. "I don't see how a taxon with a few characteristics that look like *Homo* in South Africa can be the ancestor [of *Homo*] when there's something in East Africa that is clearly *Homo* 300,000 years earlier," he declares, referring to the jaw.

Kimbel is not alone in rejecting the argument for *A. sediba* as the rootstock of *Homo.* "There are too many things that do not fit, particularly the dates and geography," comments Meave Leakey of the Turkana Basin Institute in Kenya, whose own research has focused on fossils from East Africa. "It is much more likely that the South African hominins are a separate radiation that took place in the south of the continent."

René Bobe of George Washington University says that if the *A. sediba* remains were older—say, around 2.5 million years old—they might make for a plausible *Homo* ancestor. But at 1.977 mil-



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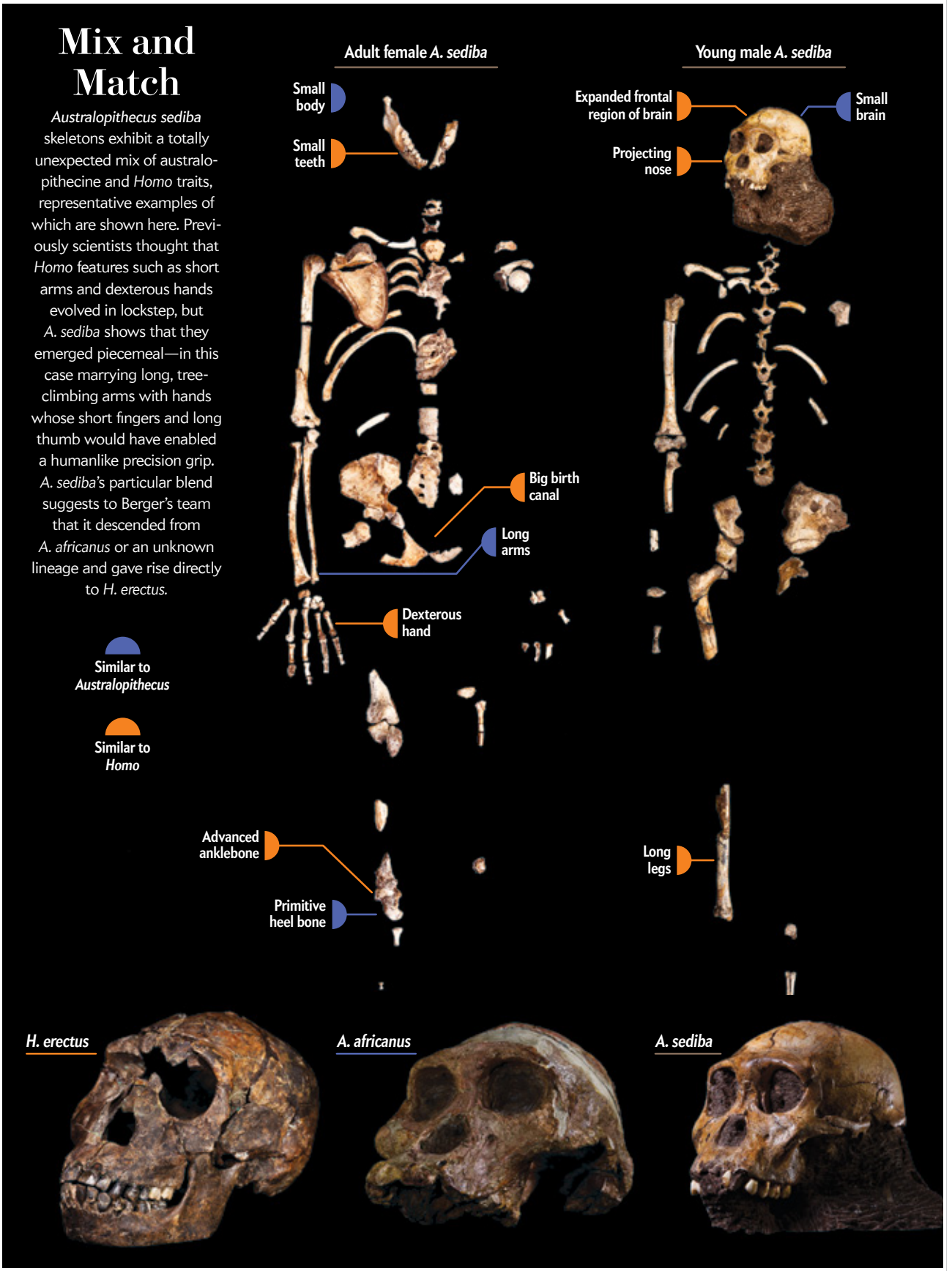
# Mix and Match

*Australopithecus sediba* skeletons exhibit a totally unexpected mix of australopithecine and *Homo* traits, representative examples of which are shown here. Previously scientists thought that *Homo* features such as short arms and dexterous hands evolved in lockstep, but *A. sediba* shows that they emerged piecemeal—in this case marrying long, tree-climbing arms with hands whose short fingers and long thumb would have enabled a humanlike precision grip. *A. sediba*'s particular blend suggests to Berger's team that it descended from *A. africanus* or an unknown lineage and gave rise directly to *H. erectus*.

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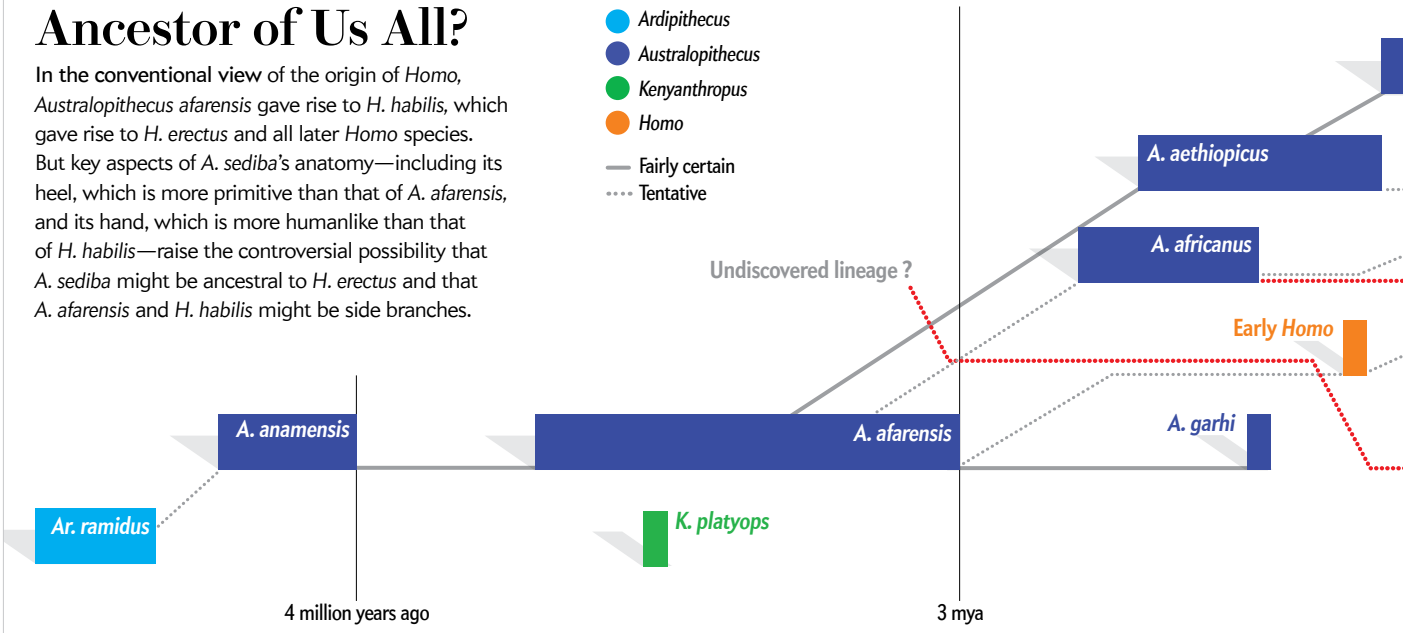
## Ancestor of Us All?

In the conventional view of the origin of *Homo*, *Australopithecus afarensis* gave rise to *H. habilis*, which gave rise to *H. erectus* and all later *Homo* species. But key aspects of *A. sediba*'s anatomy—including its heel, which is more primitive than that of *A. afarensis*, and its hand, which is more humanlike than that of *H. habilis*—raise the controversial possibility that *A. sediba* might be ancestral to *H. erectus* and that *A. afarensis* and *H. habilis* might be side branches.




lion years old, they are just too primitive in their overall form to be ancestral to fossils from Kenya's Lake Turkana region that are just a tad younger yet have many more indisputable *Homo* traits. Berger counters that *A. sediba* almost certainly existed as a species before the Malapa individuals. Bobe and others maintain that such information is not currently known. "Paleoanthropologists tend to think of the fossils they find as being in a key position within the [hominin] phylogenetic tree, and in many cases that's unlikely to be the situation," Bobe observes. From a statistical standpoint, "if you have [hominin] populations distributed across Africa, evolving in complex ways, why would the one you find be the ancestor?"

Berger has found a sympathetic ear in Wood, who says Berger is "absolutely right" that *A. sediba* demonstrates that isolated bones do not predict what the rest of the animal looks like. *A. sediba* shows that the combinations of traits evident from previous fossil discoveries do not exhaust the possibilities, Wood remarks. But he does not endorse the suggestion that *A. sediba* is the ancestor of *Homo*. "There are not many characters linking it to *Homo*," he notes, and *A. sediba* may have evolved those traits independently from the *Homo* lineage. "I just think *sediba* has got too much to do in order to evolve into [*erectus*]," Wood says.

Resolution of the issue of where *A. sediba* belongs in our family tree is hampered by the lack of a clear definition of the genus *Homo*. Coming up with one, however, is a taller order than it might seem. With so few specimens from the transition period, and most of them being scraps, identifying those features that first distinguished *Homo* from its australopithecine forebearers—those traits that made us truly human—has proved challenging. The skeletons from Malapa expose just how vexing the situation is: they are so much more complete than any early *Homo* specimen that it is very difficult to compare them with anything. "*Sediba* may force us to come up with a definition," Berger says.

**Populations are incredibly rare in the human fossil record, and the Malapa individuals have the added benefit of peerless preservation.**

### ALL IN THE DETAILS

WHATEVER THE POSITION of the Malapa fossils in the family tree, they are poised to provide researchers with the most detailed portrait yet of an early hominin species, in part because they make up multiple individuals. In addition to the juvenile male and the adult female, the two most complete specimens, Berger's team has collected bones representing another four individuals, including a baby. Populations are incredibly rare in the human fossil record, and the individuals at Malapa have the added benefit of peerless preservation. Hominin bones that virtually never survive the ravages of deep time have turned up here: a paper-thin shoulder blade, the delicate sliver that is the first rib, pea-size finger bones, vertebrae with spiny projections intact. And a number of bones that were previously known only from fragments are complete.

Before the discovery of Malapa, paleoanthropologists did not have a single complete arm from an early hominin, meaning that the limb lengths that are used to reconstruct such essential behaviors as locomotion are estimates. Even Lucy—the most complete hominin of such antiquity back when she was found in 1974—is missing significant chunks of her arm and leg bones. In the adult female from Malapa, in contrast, virtually the entire upper limb is preserved—from shoulder blade to hand. Only the very last digits of some of



*Graphic by Jen Christiansen*

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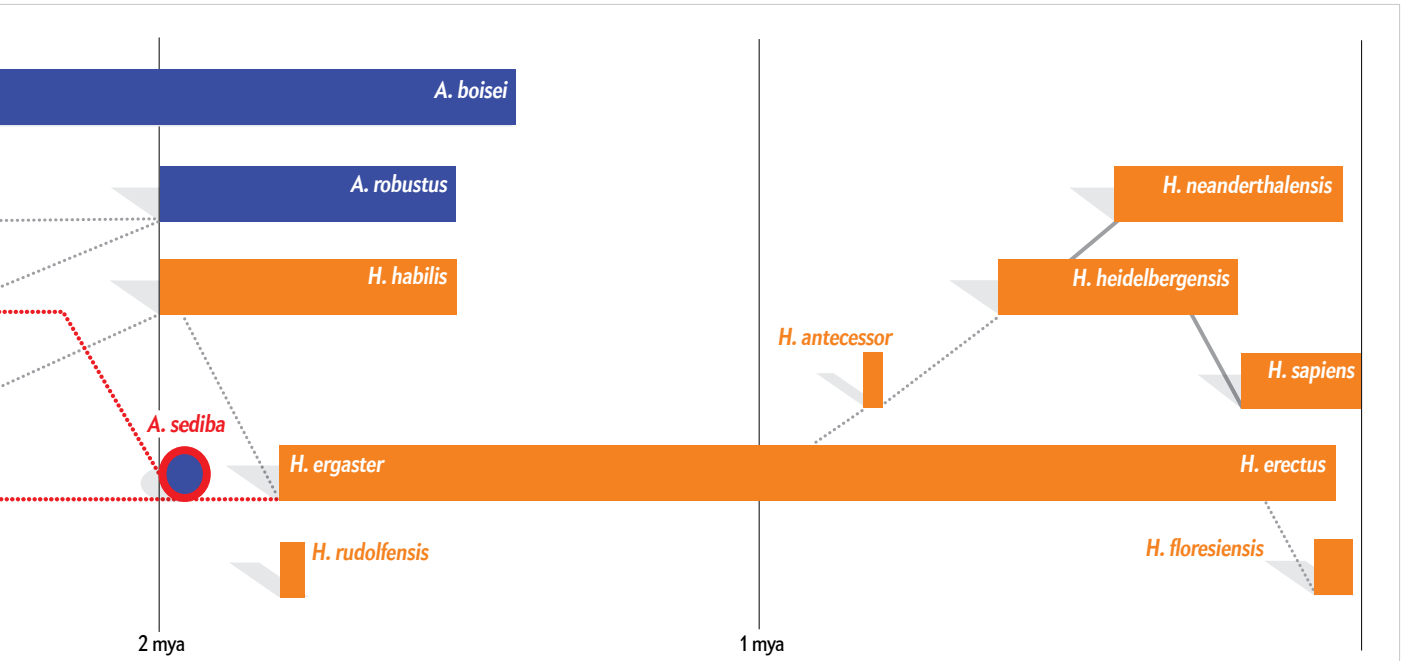


her fingers and some wristbones are missing, and Berger expects to find those—and the rest of the bones of both skeletons—when he begins systematically excavating the site. (Thus far the team has collected only bones visible from the surface.) In fact, some of the missing bones of the young male may have already turned up. In July, Berger announced that CT scanning of a large rock from the site revealed a number of bones inside, including parts of a lower jaw and possibly a complete femur. Together the Malapa fossils will enable researchers to reconstruct how *A. sediba* matured, how it moved around the landscape, and how members of the population differed from one another.

It is not only the bones that promise to furnish vital clues to our newfound relative's way of life. Malapa has also yielded some other materials that could literally flesh out researchers' understanding of *A. sediba*. Paleontologists have long thought that during the fossilization process, all of an organism's organic components—such as skin, hair, organs, and so forth—are lost to decomposition, leaving behind only mineralized bone. But when Berger saw a CT scan of the skull of the young male, he noticed a place on the crown where there appeared to be an air space between the surface of the fossil and the contour of the actual bone. Examining the spot more closely, he observed a distinctive pattern on the surface that looked like the structural components of skin. He is now conducting extensive tests to determine whether the odd-looking patch on the male's crown and another on the female's chin are in fact skin.

Preserved skin, if confirmed as such, could reveal *A. sediba*'s coloring and the density and patterning of its hair. Such evidence could also show the distribution of sweat glands—information that would provide insights into how well the species was able to regulate its body temperature, which in turn would have affected how active it was. Sweat glands could additionally offer clues to brain evolution: an effective means of keeping cool was a prerequisite for the emergence of large brain size—a trademark characteristic of *Homo*—because brains are temperature-sensitive. And if organic material is present, Berger might even be able to obtain DNA from the remains. Currently the oldest hominin DNA to have been sequenced is 100,000-year-old DNA from a Neandertal. But because the preservation conditions at Malapa were apparently exceptional, Berger has some hope of getting genetic information from the much older *A. sediba* specimens. In that event, scientists might be able to determine whether the adult female and young male really were mother and son, as has been suggested, and how, if at all, the other hominins at the site fit in. Moreover, such a discovery would prompt researchers at other early hominin sites to test for DNA, which, if successful, could settle debates over how the various hominin species were related.

Preservation of organic remains would be a first in hominin paleontology, and the Malapa team knows it will need extraordinary evidence to persuade the research community of such a claim. Yet similar claims have been made for organic material from dinosaur bones, and those are tens of millions of years older than the Malapa fossils. Organic preservation in hominin assemblages might even be fairly common, Berger suggests—it is just that no one ever thought to look for it.

Another thing no one thought to look for in a hominin this old? Tartar. The surfaces of the young male's molar teeth bear dark brown stains. Fossil preparators typically clean off the teeth when readying hominin remains for study. But Berger realized that the stains were actually the same gunk we modern humans fend off with toothbrushes and pilgrimages to the dentist. Analyses of the stains, together with studies of the tooth chemistry and wear marks, revealed that *A. sediba* had a surprising diet.

In a review paper published in *Science* in October 2011, Peter S. Ungar of the University of Arkansas and Matt Sponheimer of the University of Colorado at Boulder observed that recent analyses have hinted at unexpected dietary diversity. Studies of



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what early humans ate have looked at carbon isotope ratios in teeth, which can indicate whether an animal dined on so-called C3 plants, such as trees and shrubs; C4 plants, such as certain grasses and sedges; or some combination thereof—or, in the case of carnivorous species, preyed on animals that ate those plants. Whereas *Ardipithecus ramidus,* one of the earliest putative hominins, dined primarily on C3 foods, as savanna chimpanzees do, other early African hominins appear to have eaten a mix of C3 and C4 foods. One species, *Paranthropus robustus,* even ate a mostly C4 diet, as Thure Cerling of the University of Utah and his colleagues reported in June 2011 in the *Proceedings of the National Academy of Sciences USA*.

Analyses of *A. sediba*'s teeth add another facet to this diversity. In a paper published online by *Nature* in June, Berger, Amanda Henry of the Max Planck Institute for Evolutionary Anthropology in Leipzig and their colleagues reported that the tooth chemistry of the two most complete individuals from the site indicated a diet heavy in C3 foods. This result came as a surprise, not only because other hominins that lived around this time relied more heavily on C4 foods but because paleoecological evidence indicates that C4 plants dominated the Malapa environment. The tartar results only deepened the enigma. The team studied silica crystals called phytoliths that are embedded in the tartar. Phytoliths come from plants, and some make spe-

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**SYNCHROTRON X-RAY SCAN** of the skull of the young male *A. sediba* enabled detailed reconstruction of the brain (*pink*), which exhibits advanced reorganization in the frontal lobes despite being little larger than a chimpanzee's brain.

cies-specific forms of the crystals. Studies of these phytoliths can thus reveal exactly which kinds of plants an animal ate just before it died. *A. sediba* apparently supped on a wide variety of plant foods, including bark—not an item researchers expected to find on an early hominin menu. The wear pattern on the teeth, meanwhile, is consistent with the consumption of some hard foods shortly before death.

Taken together, the diet findings suggest to the researchers that *A. sediba* foraged for C3 foods in forests surrounded by C4 grasslands. The bark evidence could indicate that the hominins were under stress because other primates are known to eat bark when fruit and other high-quality plant foods are not available. Could the C3 signature indicate that these hominins ate animals that ate C3 plants? A taste for animal flesh could fit with the hominin's small teeth, which are typically associated with a higher-quality diet, as well as its dexterous hand, which would have been well suited to making and wielding stone tools for processing meat.

## END OF DAYS

THE FINAL DAYS of the Malapa hominins appear to have been grim ones. Possible drought conditions may have made water hard to come by. Berger suspects that the hominins, desperate for a drink, may have tried to climb down into the then 30- to 50-meter-deep underground cavern at Malapa to access a shallow pool and, in so doing, tumbled to their deaths. Perhaps the boy fell in first, and the adult female—maybe his mother—tried to rescue him only to fall in herself. A menagerie of other beasts, from antelopes to zebras, met the same fate.

Intriguingly, geologic evidence from the site indicates that the fossil assemblage at Malapa formed right around the same time that the earth was undergoing a geomagnetic reversal—a mysterious event in which the planet's polarity flips and magnetic north becomes magnetic south. The timing raises the question of whether the reversal somehow played a role in the demise of these creatures.

Scientists know very little about why reversals occur and whether they precipitate environmental change. Some geologists have suggested that these events could conceivably wreak ecological havoc. As one of the only places in the world that has a terrestrial record of a reversal and a collection of fossils from the same time, Malapa could offer rare insights into what happens when the planet's poles trade places.

Other evidence might throw additional light on their deaths. The fossilized bones of a pregnant antelope and her fetus from Malapa could help scientists pinpoint the time of year that the hominins died to within a couple of weeks: antelopes give birth within a very narrow interval in the spring, and analysis of the fetus should allow researchers to figure out how far along the antelope was before she died. Meanwhile traces of maggots and carrion beetles that set on the hominins after death could reveal how long the bodies were exposed before the cave's flowing sediments buried them.

In a sense, the work on *A. sediba* has only just begun. "You're walking all over hominin fossils," Berger tells visitors to Malapa on an austral spring morning in late November 2011. They are standing on the rocky ground between the tree where Matthew found the clavicle and the mining pit where Berger found its owner. Climbing down into the pit, he points onlookers to bits of fossils peeking out of the rock. The awestruck guests crane to glimpse an infant's arm bone and the lower jaw of a false saber-toothed cat. Just by gathering remains exposed by the miners and the occasional rainstorm, the team has amassed one of the largest fossil hominin samples on record. Once the researchers begin excavating the roughly 500-square-meter site, Berger knows they will find more bones—many more. Extensive planning is under way to erect a structure to protect the site from the elements and serve as a state-of-the-art field laboratory. Meanwhile, in the Malapa block lab at the University of the Witwatersrand, chunks of rock blasted from the miners' pit fill floor-to-ceiling shelves. Researchers are peering into the rocks with a CT scanner to look for more hominin bones, including the adult female's missing skull.

So vast are Malapa's riches that Berger could probably spend the rest of his career working on them. Yet already he is thinking about where he wants to go next. *A. sediba* "has taught me that we really need a better record—and it's out there," he warrants. The mapping project that led Berger to Malapa identified more than three dozen new sites in the Cradle alone that could potentially harbor hominin remains. He is lining up researchers to dig the most promising of those spots. Berger himself has his sights set farther afield. The Congo and Angola have caves similar to the ones in the Cradle and have never been searched for hominin fossils, he observes. Perhaps there he will find another unexpected emissary from the dawn of humankind that will rewrite the story of our origins once again. SA

**KATE WONG** is a senior editor at *Scientific American*.

MORE TO EXPLORE

*Australopithecus sediba:* A New Species of *Homo*-like Australopith from South Africa. Lee R. Berger et al. in *Science*, Vol. 328, pages 195–204; April 9, 2010.

The September 9, 2011, issue of *Science* contains five research papers on details of *A. sediba*'s anatomy and age.



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BIOLOGY

# The Naked Truth

## Our nearly hairless skin was a key factor in the emergence of other human traits

**BY NINA G. JABLONSKI**

AMONG PRIMATES, HUMANS ARE UNIQUE IN having nearly naked skin. Every other member of our extended family has a dense covering of fur—from the short, black pelage of the howler monkey to the flowing copper coat of the orangutan—as do most other mammals. Yes, we humans have hair on our heads and elsewhere, but compared with our relatives, even the hairiest person is basically bare.

How did we come to be so denuded? Scholars have pondered this question for centuries. Finding answers has been difficult, however: most of the hallmark transitions in human evolution—such as the emergence of upright walking—are recorded directly in the fossils of our predecessors, but none of the known remains preserves irrefutable impressions of human skin. In recent years, though, researchers have realized that the fossil record does contain indirect hints about our transformation from hirsute to hairless. Thanks to these clues and insights gleaned over the past decade from genomics and physiology, I and others have pieced together a compelling account of why and when humans shed their fur. In addition to explaining a very peculiar quirk of our appearance, the scenario suggests that naked skin itself played a crucial role in the evolution of other characteristic human traits, including our large brain and dependence on language.

### HAIRY SITUATIONS

TO UNDERSTAND WHY our ancestors lost their body hair, we must first consider why other species have coats in the first place. Hair is a type of body covering that is unique to mammals. Indeed, it is a defining characteristic of the class: all mammals possess at least some hair, and most of them have it in abundance. It provides insulation and protection against abrasion, moisture, damaging rays of sunlight, and potentially harmful parasites and microbes. It also works as camouflage to confuse predators, and its distinctive patterns allow members of the same species to recognize one another. Furthermore, mammals can use their fur in social displays to indicate aggression or agitation: when a dog "raises its hackles" by involuntarily elevating the hairs on its neck and back, it is sending a clear signal to challengers to stay away.

Yet even though fur serves these many important purposes, a number of mammal lineages have evolved hair that is so sparse and fine as to serve no function. Many of these creatures live underground or dwell exclusively in the water. In subterranean mammals, such as the naked mole rat, hairlessness evolved as a response to living in large underground colonies, where the benefits of hair are superfluous because the animals cannot see one

**IN BRIEF**

**Humans** are the only primate species that has mostly naked skin.
**Loss of fur** was an adaptation to changing environmental conditions that forced our ancestors to travel longer distances for food and water.
**Analyses** of fossils and genes hint at when this transformation to bare skin occurred.
**The evolution** of hairlessness made way for the emergence of large brains and symbolic thought.

DORIT THIES



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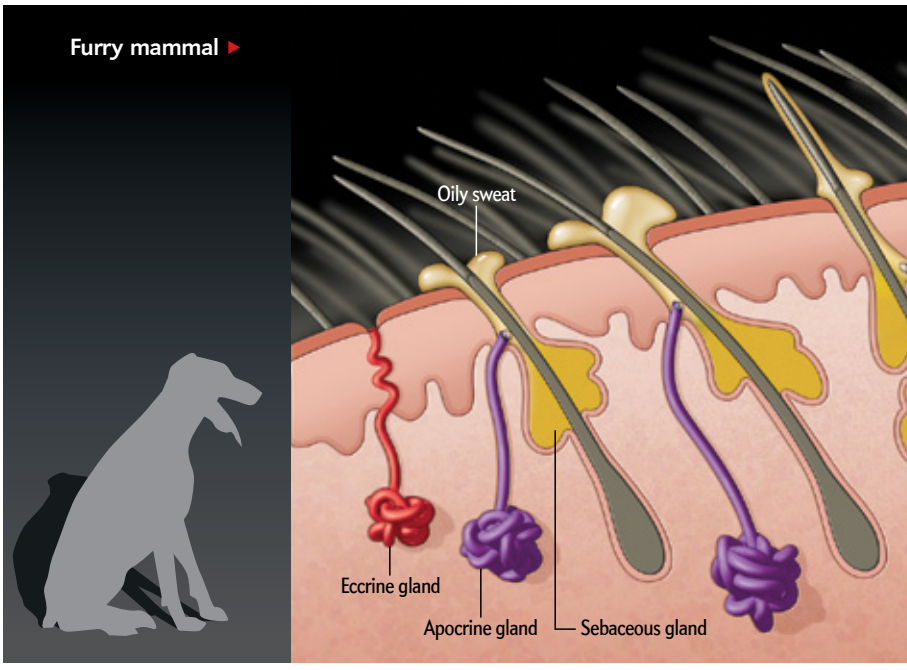
# Furry vs. Naked

**Naked human skin** is better at ridding the body of excess heat than is fur-covered skin. Mammals possess three types of glands for the purpose: apocrine, eccrine and sebaceous. In most mammals the outermost layer of the skin, known as the epidermis, contains an abundance of apocrine glands. These glands cluster around hair follicles and coat the fur in a lather of oily sweat. Evaporation of this sweat, which cools the animal by drawing heat away from the skin, occurs at the surface of the fur. But the more the animal perspires, the less effectively it eliminates heat because the fur becomes matted, hampering evaporation. In the human epidermis, in contrast, eccrine glands predominate. These glands reside close to the skin surface and discharge thin, watery sweat through tiny pores. In addition to evaporating directly from the skin surface, this eccrine sweat vaporizes more readily than apocrine sweat, thus permitting improved cooling.




another in the dark and because their social structure is such that they simply huddle together for warmth. In marine mammals that never venture ashore, such as whales, naked skin facilitates long-distance swimming and diving by reducing drag on the skin's surface. To compensate for the lack of external insulation, these animals have blubber under the skin. In contrast, semiaquatic mammals—otters, for example—have dense, waterproof fur that traps air to provide positive buoyancy, thus decreasing the effort needed to float. This fur also protects their skin on land.

The largest terrestrial mammals—namely, elephants, rhinoceroses and hippopotamuses—also evolved naked skin because they are at constant risk of overheating. The larger an animal is, the less surface area it has relative to overall body mass and the harder it is for the creature to rid its body of excess heat. (On the flip side, mice and other small animals, which have a high surface-to-volume ratio, often struggle to retain sufficient heat.) During the Pleistocene epoch, which spans the time between two million and 10,000 years ago, the mammoths and other relatives of modern elephants and rhinoceroses were "woolly" because they lived in cold environments, and external insulation helped them conserve body heat and lower their food intake. But all of today's megaherbivores live in sweltering conditions, where a fur coat would be deadly for beasts of such immense proportions.

Human hairlessness is not an evolutionary adaptation to living underground or in the water—the popular embrace of the so-called aquatic ape hypothesis notwithstanding [*see box on page 26*]. Neither is it the result of large body size. But our bare skin is related to staying cool, as our superior sweating abilities suggest.

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## SWEATING IT OUT

KEEPING COOL is a big problem for many mammals, not just the giant ones, especially when they live in hot places and generate abundant heat from prolonged walking or running. These animals must carefully regulate their core body temperature because their tissues and organs, specifically the brain, can become damaged by overheating.

Mammals employ a variety of tactics to avoid burning up: dogs pant, many cat species are most active during the cooler evening hours, and many antelopes can off-load heat from the blood in their arteries to blood in small veins that has been cooled by breathing through the nose. But for primates, including humans, sweating is the primary strategy. Sweating cools the body through the production of liquid on the skin's surface that then evaporates, drawing heat energy away from the skin in the process. This whole-body cooling mechanism operates according to the same principle as an evaporative cooler (also known as a swamp cooler), and it is highly effective in preventing the dangerous overheating of the brain, as well as of other body parts.

Not all sweat is the same, however. Mammalian skin contains three types of glands—sebaceous, apocrine and eccrine—that together produce sweat. In most species, sebaceous and apocrine glands are the dominant sweat glands and are located near the base of hair follicles. Their secretions combine to coat hairs with an oily, sometimes foamy, mixture (think of the lather a racehorse generates when it runs). This type of sweat helps to cool the animal. But its ability to dissipate heat is limited. G. Edgar Folk, Jr., of the University of Iowa and his colleagues showed nearly two decades ago that the effectiveness of cooling diminishes as an animal's coat becomes wet and

TAMI TOLPA (*skin cross sections*); JEN CHRISTIANSEN (*dog and human*)



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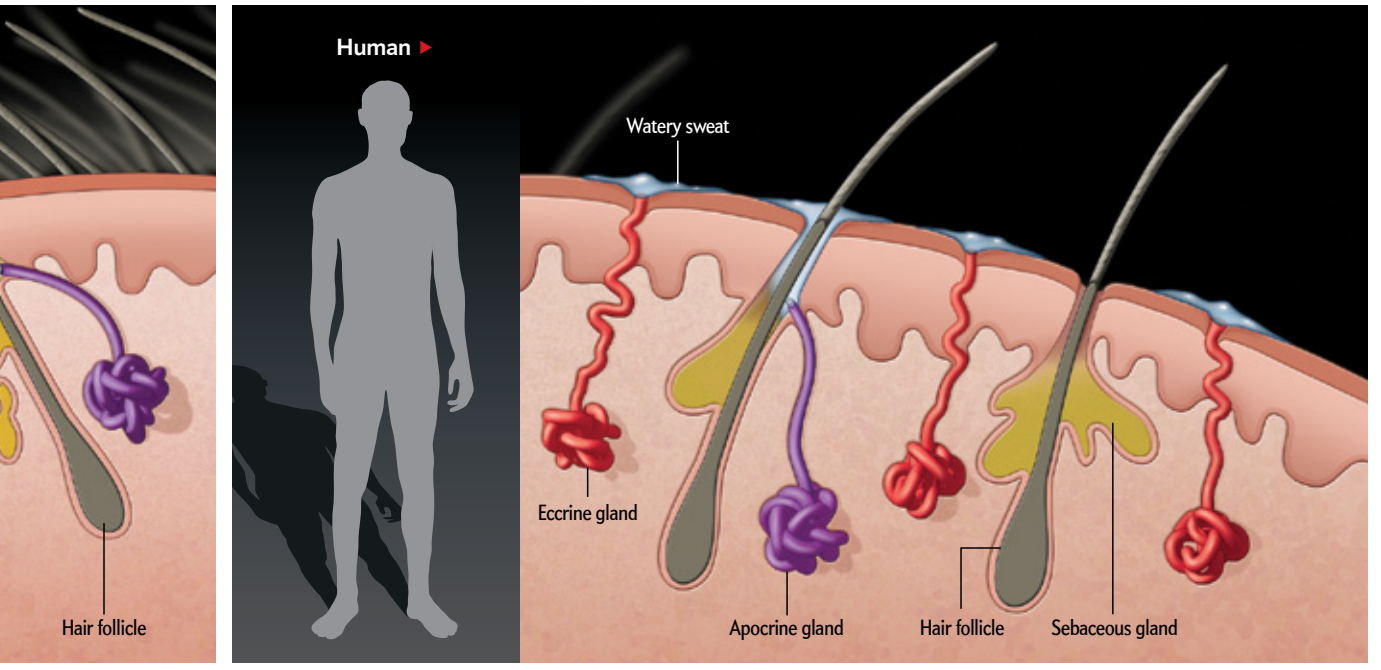


matted with this thick, oily sweat. The loss of efficiency arises because evaporation occurs at the surface of the fur, not at the surface of the skin itself, thus impeding the transfer of heat. Under conditions of duress, heat transfer is inefficient, requiring that the animal drink large amounts of water, which may not be readily available. Fur-covered mammals forced to exercise energetically or for prolonged periods in the heat of day will collapse from heat exhaustion.

Humans, in addition to lacking fur, possess an extraordinary number of eccrine glands—between two million and five million—that can produce up to 12 liters of thin, watery sweat a day. Eccrine glands do not cluster near hair follicles; instead they reside relatively close to the surface of the skin and discharge sweat through tiny pores. This combination of naked skin and watery sweat that sits directly atop it rather than collecting in the fur allows humans to eliminate excess heat very efficiently. In fact, according to a 2007 paper in *Sports Medicine* by Daniel E. Lieberman of Harvard University and Dennis M. Bramble of the University of Utah, our cooling system is so superior that in a marathon on a hot day, a human could outcompete a horse.

## BEATING THE HEAT

**Naked skin is not** the only adaptation humans evolved to maintain a healthy body temperature in the sweltering tropics where our ancestors lived. They also developed longer limbs, increasing their surface-to-volume ratio, which in turn facilitated the loss of excess heat. That trend seems to be continuing even today. The best evidence of this sustained adaptation comes from populations in East Africa, such as the Dinka of southern Sudan. It is surely no coincidence that these people, who live in one of the hottest places on earth, also have extremely long limbs.

Why do modern humans exhibit such a wide range of limb proportions? As our forebearers migrated out of tropical Africa into cooler parts of the world, the selection pressures changed, allowing for a variety of body shapes to evolve.

### SHOWING SOME SKIN

BECAUSE HUMANS are the only primates that lack coats and have an abundance of eccrine glands, something must have happened since our hominid lineage diverged from the line leading to our closest living relative, the chimpanzee, that favored the emergence of naked, sweaty skin. Perhaps not surprisingly, the transformation seems to have begun with climate change. By using fossils of animals and plants to reconstruct ancient ecological conditions, scientists have determined that starting around three million years ago the earth entered into a phase of global cooling that had a drying effect in East and Central Africa, where human ancestors lived. With this decline in regular rainfall, the wooded environments favored by early hominids gave way to open savanna grasslands, and the foods that our ancestors the australopithecines subsisted on—fruits, leaves, tubers and seeds—became scarcer, more patchily distributed and subject to seasonal availability, as did permanent sources of freshwater. In response to this dwindling of resources, our forebearers would have had to abandon their relatively leisurely foraging habits for a much more consistently active way of life just to stay hydrated and obtain enough calories, traveling ever longer distances in search of water and edible plant foods.

It is around this time that hominids also began incorporating meat into their diet, as revealed by the appearance of stone tools and butchered animal bones in the archaeological record around 2.6 million years ago. Animal foods are considerably richer in calories than are plant foods, but they are rarer on the land-



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scape. Carnivorous animals therefore need to range farther and wider than their herbivorous counterparts to procure a sufficient amount of food. Prey animals are also moving targets, save for the occasional carcass, which means predators must expend that much more energy to obtain their meal. In the case of human hunters and scavengers, natural selection morphed the apelike proportions of the australopithecines, who still spent some time in the trees, into a long-legged body built for sustained striding and running. (This modern form also no doubt helped our ancestors avoid becoming dinner themselves when out in the open.)

But these elevated activity levels came at a price: a greatly increased risk of overheating. Beginning in the 1980s, Peter Wheeler of Liverpool John Moores University in England published a series of papers in which he simulated how hot ancestral humans would have become out on the savanna. Wheeler's work, together with research my colleagues and I published in 1994, shows that the increase in walking and running, during which muscle activity builds up heat internally, would have required that hominids both enhance their eccrine sweating ability and lose their body hair to avoid overheating.

When did this metamorphosis occur? Although the human fossil record does not preserve skin, researchers do have a rough idea of when our forebearers began engaging in modern patterns of movement. Studies conducted independently by Lieberman and Christopher Ruff of Johns Hopkins University have shown that by about 1.6 million years ago an early member of our genus called *Homo ergaster* had evolved essentially modern body proportions, which would have permitted prolonged walking and running. Moreover, details of the joint surfaces of the ankle, knee and hip make clear that these hominids actually exerted themselves in this way. Thus, according to the fossil evidence, the transition to naked skin and an eccrine-based sweating system must have been well under way by 1.6 million years ago to offset the greater heat loads that accompanied our predecessors' newly strenuous way of life.

**Going furless was not merely a means to an end; it had profound consequences for subsequent phases of human evolution.**

Another clue to when hominids evolved naked skin has come from investigations into the genetics of skin color. In an ingenious study published in 2004, Alan R. Rogers of the University of Utah and his colleagues examined sequences of the human *MC1R* gene, which is among the genes responsible for producing skin pigmentation. The team showed that a specific gene variant always found in Africans with dark pigmentation originated as many as 1.2 million years ago. Early human ancestors are believed to have had pinkish skin covered with black fur, much as chimpanzees do, so the evolution of permanently dark skin was presumably a requisite evolutionary follow-up to the loss of our sun-shielding body hair. Rogers's estimate thus provides a minimum age for the dawn of nakedness.

### SKIN DEEP

LESS CERTAIN THAN WHY and when we became naked is how hominids evolved bare flesh. The genetic evidence for the evolution of nakedness has been difficult to locate because many genes contribute to the appearance and function of our skin. Nevertheless, hints have emerged from large-scale comparisons of the sequences of DNA "code letters," or nucleotides, in the entire genomes of different organisms. Comparison of the human and

ALTERNATIVE IDEAS

## Why the Aquatic Ape Theory Doesn't Hold Water

Among the many theories that attempt to explain the evolution of naked skin in humans, the aquatic ape theory (AAT)—which posits that humans went through an aquatic phase in their evolution—has attracted the most popular attention and support. First enunciated by English zoologist Sir Alister Hardy in a popular scientific article in 1960, the AAT later found a champion in writer Elaine Morgan, who continues to promote the theory in her lectures and writings. The problem is, the theory is demonstrably wrong.

The AAT holds that around five million to seven million years ago tectonic upheavals in the Rift Valley of East Africa cut early human ancestors off from their preferred tropical forest environments. As a result, they had to adapt to a semiaquatic life in marshes, along coasts and in floodplains, where they lived for about a million years. Evidence of this aquatic phase, Morgan argues, comes from several anatomical features humans share with aquatic and semiaquatic mammals but not with savanna mammals. These traits include our bare skin, a reduced number of apocrine glands, and fat deposits directly under the skin.

The AAT is untenable for three major reasons. First, aquatic mammals themselves differ considerably in the degree to which they exhibit Morgan's aquatic traits. Thus, there is no simple connection between, say, the amount of hair an animal has and the environment in which it lives. Second, the fossil record shows that watery habitats were thick with hungry crocodiles and aggressive hippopotamuses. Our small, defenseless ancestors would not have stood a chance in an encounter with such creatures. Third, the AAT is overly complex. It holds that our forebearers shifted from a terrestrial way of life to a semiaquatic one and then returned to living on terra firma full-time. As John H. Langdon of the University of Indianapolis has argued, a more straightforward interpretation of the fossil record is that humans always lived on land, where the driving force behind the evolution of naked skin was climate change that favored savanna grasslands over woodlands. And from a scientific perspective, the simplest explanation is usually the correct one. —*N.G.J.*



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# Ancestors on the Move

**Although the fossil record** does not preserve any indisputable evidence of ancient human skin, scientists can estimate when nakedness evolved based on other fossil clues. Protohumans such as the australopithecines (*top*) probably led relatively sedentary lives, as today's apes do, because they lived in or near wooded environments rich in plant foods and freshwater. But as woodlands shrank and grasslands expanded, later ancestors, such as *Homo ergaster* (*bottom*), had to travel ever farther in search of sustenance—including meat. This species, which arose by 1.6 million years ago, was most likely the first to possess naked skin and eccrine sweat glands, which would have offset the body heat generated by such elevated activity levels.

***Australopithecus afarensis,*** represented here by the 3.2-million-year-old Lucy fossil, was apelike in having short legs that were not well suited to traveling long distances.

***Homo ergaster*** was the first hominid to possess long, striding legs, seen here in the 1.6-million-year-old Turkana Boy skeleton. Such elongated limbs facilitated sustained walking and running.

VICTOR DEAK (*illustrations*); COURTESY OF DENIS FINNIN AND JACKIE BECKETT *American Museum of Natural History* (*Lucy* and *Turkana Boy*)



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**SOCIAL SIGNALING** is an important function of fur—from raised hackles indicating aggression to coat patterns that help members of the same species to recognize one another. We humans compensate for our lack of fur by decorating our bodies with tattoos, jewelry and other adornments. We also have complex facial expressions, as well as the ability to convey our emotions through language.

chimp genomes reveals that one of the most significant differences between chimp DNA and our own lies in the genes that code for proteins that control properties of the skin. The human versions of some of those genes encode proteins that help to make our skin particularly waterproof and scuff-resistant—critical properties, given the absence of protective fur. This finding implies that the advent of those gene variants contributed to the origin of nakedness by mitigating its consequences.

The outstanding barrier capabilities of our skin arise from the structure and makeup of its outermost layer, the stratum corneum (SC) of the epidermis. The SC has what has been described as a bricks-and-mortar composition. In this arrangement, multiple layers of flattened dead cells called corneocytes, which contain the protein keratin and other substances, are the bricks; ultrathin layers of lipids surrounding each of the corneocytes make up the mortar.

Most of the genes that direct the development of the SC are ancient, and their sequences are highly conserved among vertebrates. That the genes undergirding the human SC are so distinctive signifies, therefore, that the advent of those genes was important to survival. These genes encode the production of a unique combination of proteins that occur only in the epidermis, including novel types of keratin and involucrin. A number of laboratories are currently attempting to unravel the precise mechanisms responsible for regulating the manufacture of these proteins.

Other researchers are looking at the evolution of keratins in body hair, with the aim of determining the mechanisms responsible for the sparseness and fineness of body hair on the surface of human skin. To that end, Roland Moll of Philipps University in Marburg, Germany, and his colleagues have shown that the keratins present in human body hair are extremely fragile, which is why these hairs break so easily compared with those of other animals. This finding, detailed in a paper Moll published in 2008, suggests that human hair keratins were not as important to survival as the hair keratins of other primates were over the course of evolution and thus became weak.

Another question geneticists are eager to answer is how human skin came to contain such an abundance of eccrine glands. Almost certainly this accumulation occurred through changes in the genes that determine the fate of epidermal stem cells, which are unspecialized, in the embryo. Early in development,

HEINRICH VAN DEN BERG *Getty Images (cheetah)*; HENRY HORNSTEIN *Getty Images (tattoos)*; MARK WILSON *Getty Images (woman)*; GETTY IMAGES *(Barack Obama)*



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groups of epidermal stem cells in specific locations interact with cells of the underlying dermis, and genetically driven chemical signals within these niches direct the differentiation of the stem cells into hair follicles, eccrine glands, apocrine glands, sebaceous glands or plain epidermis. Many research groups are now investigating how epidermal stem cell niches are established and maintained, and this work should clarify what directs the fate of embryonic epidermal cells and how more of these cells become eccrine sweat glands in humans.

### NOT ENTIRELY NUDE

HOWEVER IT WAS that we became naked apes, evolution did leave a few body parts covered. Any explanation of why humans lost their fur therefore must also account for why we retain it in some places. Hair in the armpits and groin probably serves both to propagate pheromones (chemicals that serve to elicit a behavioral response from other individuals) and to help keep these areas lubricated during locomotion. As for hair on the head, it was most likely retained to help shield against excess heat on the top of the head. That notion may sound paradoxical, but having dense hair on the head creates a barrier layer of air between the sweating scalp and the hot surface of the hair. Thus, on a hot, sunny day the hair absorbs the heat while the barrier layer of air remains cooler, allowing sweat on the scalp to evaporate into that layer of air. Tightly curled hair provides the optimum head covering in this regard because it increases the thickness of the space between the surface of the hair and the scalp, allowing air to blow through. Much remains to be discovered about the evolution of human head hair, but it is possible that tightly curled hair was the original condition in modern humans and that other hair types evolved as humans dispersed out of tropical Africa.

With regard to our body hair, the question is why it is so variable. There are many populations whose members have hardly any body hair at all and some populations of hirsute folks. Those with the least body hair tend to live in the tropics, whereas those with the most tend to live outside the tropics. Yet the hair on these nontropical people provides no warmth to speak of. These differences in hairiness clearly stem to some extent from testosterone because males in all populations have more body hair than females do. A number of theories aimed at explaining this imbalance attribute it to sexual selection. For example, one posits that females prefer males with fuller beards and thicker body hair because these traits occur in tandem with virility and strength. Another proposes that males have evolved a preference for females with more juvenile features. These are interesting hypotheses, but no one has actually tested them in a modern human population; thus, we do not know, for instance, whether hairy men are in fact more vigorous or fecund than their sleeker counterparts. In the absence of any empirical evidence, it is still anybody's guess why human body hair varies the way it does.

## OF LICE AND MEN

**In recent years** researchers have looked to lice for clues to why humans lost their body hair. In 2003 Mark Pagel of the University of Reading in England and Walter Bodmer of John Radcliffe Hospital in Oxford proposed that humans shed their fur to rid their bodies of disease-spreading lice and other fur-dwelling parasites and to advertise the health of their skin. Other investigators have studied head and body lice for insight into how long after becoming bare-skinned our ancestors began to cover up with clothing.

Although body lice feed on blood, they live on clothing. Thus, the origin of body lice provides a minimum estimate for the dawn of hominid garb. By comparing gene sequences of organisms, investigators can learn roughly when the species arose. Such analyses in lice indicate that whereas head lice have plagued humans from the start, body lice evolved much later. The timing of their appearance hints that humans went naked for more than a million years before getting dressed.

### NAKED AMBITIONS

GOING FURLESS was not merely a means to an end; it had profound consequences for subsequent phases of human evolution. The loss of most of our body hair and the gain of the ability to dissipate excess body heat through eccrine sweating helped to make possible the dramatic enlargement of our most temperature-sensitive organ, the brain. Whereas the australopithecines had a brain that was, on average, 400 cubic centimeters—roughly the size of a chimp's brain—*H. ergaster* had a brain twice that large. And within a million years the human brain swelled another 400 cubic centimeters, reaching its modern size. No doubt other factors influenced the expansion of our gray matter—the adoption of a sufficiently caloric diet to fuel this energetically demanding tissue, for example. But shedding our body hair was surely a critical step in becoming brainy.

Our hairlessness also had social repercussions. Although we can involuntarily raise and lower our hackles when the small muscles at the base of our hair follicles contract and relax, our body hairs are so thin and wispy that we do not put on much of a show compared with the displays of our cats and dogs or of our chimpanzee cousins. Neither do we have the built-in advertising—or camouflage—offered by zebra stripes, leopard spots, and the like. Indeed, one might even speculate that universal human traits such as social blushing and complex facial expressions evolved to compensate for our lost ability to communicate through our fur. Likewise, body paint, cosmetics, tattoos and other types of skin decoration are found in various combinations in all cultures because they convey group membership, status and other vital social information formerly encoded by fur. We also employ body postures and gestures to broadcast our emotional states and intentions. And we use language to speak our mind in detail. Viewed this way, naked skin did not just cool us down—it made us human. SA

### MORE TO EXPLORE


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**THE 1 PERCENT DIFFERENCE:**
**Humans are distinct from chimpanzees in a number of important respects, despite sharing nearly 99 percent of their DNA. New analyses are revealing which parts of the genome set our species apart.**

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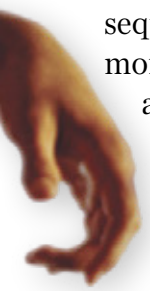
# What Makes Us Different?

Comparisons of the genomes of humans and chimpanzees are revealing those rare stretches of DNA that are ours alone

BY KATHERINE S. POLLARD



NINE YEARS AGO I JUMPED AT AN OPPORTUNITY to join the international team that was identifying the sequence of DNA bases, or "letters," in the genome of the common chimpanzee (*Pan troglodytes*). As a biostatistician with a long-standing interest in human origins, I was eager to line up the human DNA sequence next to that of our closest living relative and take stock. A humbling truth emerged: our DNA blueprints are nearly 99 percent identical to theirs. That is, of the three billion letters that make up the human genome, only 15 million of them—less than 1 percent—have changed in the six million years or so since the human and chimp lineages diverged.

Evolutionary theory holds that the vast majority of these changes had little or no effect on our biology. But somewhere among those roughly 15 million bases lay the differences that made us human. I was determined to find them. Since then, I and others have made tantalizing progress in identifying a number of DNA sequences that set us apart from chimps.

## AN EARLY SURPRISE

DESPITE ACCOUNTING for just a small percentage of the human genome, millions of bases are still a vast territory to search. To facilitate the hunt, I wrote a computer program that would scan the human genome for the pieces of DNA that have changed the most since humans and chimps split from a common ancestor. Because most random genetic mutations neither benefit nor harm an organism, they accumulate at a steady rate that reflects the amount of time that has passed since two living species had a common forebearer (this rate of change is often spoken of as the "ticking of the molecular clock"). Acceleration in that rate of change in some part of the genome, in contrast, is a hallmark of positive selection, in which mutations that help an organism survive and reproduce are more likely to be passed on to future generations. In other words, those parts of the code that have undergone the most modification since the chimp-human split are the sequences that most likely shaped humankind.

In November 2004, after months of debugging and optimizing my program to run on a massive computer cluster at the University of California, Santa Cruz, I finally ended up with a file that contained a ranked list of these rapidly evolving sequences. With my mentor David Haussler leaning over my shoulder,

JAMES BALOG Getty Images

**IN BRIEF**

**Chimpanzees** are the closest living relatives of humans and share nearly 99 percent of our DNA. **Efforts to identify** those regions of the human genome that have changed the most since chimps and humans diverged from a common ancestor have helped pinpoint the DNA sequences that make us human. **The findings** have also provided vital insights into how chimps and humans can differ so profoundly, despite having nearly identical DNA blueprints.



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I looked at the top hit, a stretch of 118 bases that together became known as human accelerated region 1 (HAR1). Using the U.C. Santa Cruz genome browser, a visualization tool that annotates the human genome with information from public databases, I zoomed in on HAR1. The browser showed the HAR1 sequences of a human, chimp, mouse, rat and chicken—all of the vertebrate species whose genomes had been decoded by then. It also revealed that previous large-scale screening experiments had detected HAR1 activity in two samples of human brain cells, although no scientist had named or studied the sequence yet. We yelled, "Awesome!" in unison when we saw that HAR1 might be part of a gene new to science that is active in the brain.

We had hit the jackpot. The human brain is well known to differ considerably from the chimpanzee brain in terms of size, organization and complexity, among other traits. Yet the developmental and evolutionary mechanisms underlying the characteristics that set the human brain apart are poorly understood. HAR1 had the potential to illuminate this most mysterious aspect of human biology.

We spent the next year finding out all we could about the evolutionary history of HAR1 by comparing this region of the genome in various species, including 12 more vertebrates that were sequenced during that time. It turns out that until humans came along, HAR1 evolved extremely slowly. In chickens and chimps—whose lineages diverged some 300 million years ago—only two of the 118 bases differ, compared with 18 differences between humans and chimps, whose lineages diverged far more recently. The fact that HAR1 was essentially frozen in time through hundreds of millions of years indicates that it does something very important; that it then underwent abrupt revision in humans suggests that this function was significantly modified in our lineage.

A critical clue to the function of HAR1 in the brain emerged in 2005, after my collaborator Pierre Vanderhaeghen of the Free University of Brussels obtained a vial of HAR1 copies from our laboratory during a visit to Santa Cruz. He used these DNA sequences to design a fluorescent molecular tag that would light up when HAR1 was activated in living cells—that is, copied from DNA into RNA. When typical genes are switched on in a cell, the cell first makes a mobile messenger RNA copy and then uses the RNA as a template for synthesizing some needed protein. The labeling revealed that HAR1 is active in a type of neuron that plays a key role in the pattern and layout of the developing cerebral cortex, the wrinkled outermost brain layer. When things go wrong in these neurons, the result may be a severe, often deadly, congenital disorder known as lissencephaly ("smooth brain"), in which the cortex lacks its characteristic folds and exhibits a markedly reduced surface area. Malfunctions in these same neurons are also linked to the onset of schizophrenia in adulthood.

HAR1 is thus active at the right time and place to be instrumental in the formation of a healthy cortex. (Other evidence suggests that it may additionally play a role in sperm production.) But exactly how this piece of the genetic code affects cortex development is a mystery my colleagues and I are still trying to solve. We are eager to do so: HAR1's recent burst of substitutions may have altered our brains significantly.

**You do not need to change very much of the genome to make a new species.**

Beyond having a remarkable evolutionary history, HAR1 is special because it does not encode a protein. For decades, molecular biology research focused almost exclusively on genes that specify proteins, the basic building blocks of cells. But thanks to the Human Genome Project, which sequenced our own genome, scientists now know that protein-coding genes make up just 1.5 percent of our DNA. The other 98.5 percent—sometimes referred to as junk DNA—contains regulatory sequences that tell other genes when to turn on and off and genes encoding RNA that does not get translated into a protein, as well as a lot of DNA having purposes scientists are only beginning to understand.

Based on patterns in the HAR1 sequence, we predicted that HAR1 encodes RNA—a hunch that Sofie Salama, Haller Igel and Manuel Ares, all at U.C. Santa Cruz, subsequently confirmed in 2006 through lab experiments. In fact, it turns out that human HAR1 resides in two overlapping genes. The shared HAR1 sequence gives rise to an entirely new type of RNA structure, adding to the six known classes of RNA genes. These six major groups encompass more than 1,000 different families of RNA genes, each one distinguished by the structure and function of the encoded RNA in the cell. HAR1 is also the first documented example of an RNA-encoding sequence that appears to have undergone positive selection.

It might seem surprising that no one paid attention to these amazing 118 bases of the human genome earlier. But in the absence of technology for readily comparing whole genomes, researchers had no way of knowing that HAR1 was more than just another piece of junk DNA.

**KATHERINE S. POLLARD** is a biostatistician at the Gladstone Institutes at the University of California, San Francisco. In 2003, after completing a Ph.D. and postdoctoral research at U.C. Berkeley, she began a comparative genomics fellowship at U.C. Santa Cruz, during which she participated in the sequencing of the chimpanzee genome. Pollard used this sequence to identify the fastest-evolving regions of the human genome. A recipient in 2008 of a Sloan Research Fellowship, she recently began studying the evolution of microbes that live in the human body.

## LANGUAGE CLUES

WHOLE-GENOME COMPARISONS in other species have also provided another crucial insight into why humans and chimps can be so different despite being much alike in their genomes. In the past decade the genomes of thousands of species (mostly microbes) have been sequenced. It turns out that *where* DNA substitutions occur in the genome—rather than how many changes arise overall—can matter a great deal. In other words, you do not need to change very much of the genome to make a new species. The way to evolve a human from a chimp-human ancestor is not to speed the ticking of the molecular clock as a whole. Rather the secret is to have rapid change occur in sites where those changes make an important difference in an organism's functioning.

HAR1 is certainly such a place. So, too, is the *FOXP2* gene, which contains another of the fast-changing sequences I identified and is known to be involved in speech. Its role in speech was dis-



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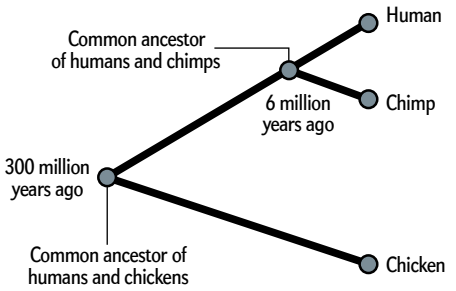
EXPERIMENT

# Scanning the Genome

**To find the parts** of our genome that make us human, the author wrote a computer program that searched for the DNA sequences that have changed the most since humans and chimpanzees diverged from their last common ancestor. Topping the list was a 118-letter snippet of code known as human accelerated region 1 (HAR1). This region of the genome changed very little for most of vertebrate evolution, with chimp and chicken sequences differing by just two letters. Human and chimp HAR1s, however, differ by 18 letters, suggesting that HAR1 acquired an important new function in humans.




T G A A A **C** G G A G G A G A **C G** T T A C
A G C A A **C G** T **G** T C A **G** C T G A A A T
**G** A T **G** G G **C** G T A G A C **G** C A **C** G T C
A G C **G** G **C** G G A A A T **G** G T T T C T A
T C A A A A T **G** A A A G T **G** T T T A G A
G A T T T T C C T C A A **G** T T T C A

**■** Changes in human sequence relative to that of the chimp

T G A A A T G G A G G A G A A A T T A C
A G C A A T T T A T C A A C T G A A A T
T A T A G G T G T A G A C A C A T G T C
A G C A G T **G** G A A A **T** A G T T T C T A
T C A A A A T T A A A A G T A T T T A G A
G A T T T T C C T C A A A T T T C A

**■** Changes in chimp sequence relative to that of the chicken

T G A A A T G G A G G A G A A A T T A C
A G C A A T T T A T C A A C T G A A A T
T A T A G G T G T A G A C A C A T G T C
A G C A G T G G A A A T A G T T T C T A
T C A A A A T T A A A A G T A T T T A G A
G A T T T T C C T C A A A T T T C A

One finding has shed some light on when the speech-enabling version of *FOXP2* appeared in hominids: in 2007 scientists at the Max Planck Institute for Evolutionary Anthropology in Leipzig sequenced *FOXP2* extracted from a Neandertal fossil and found that these extinct humans had the modern human version of the gene, perhaps permitting them to enunciate as we do. Current estimates for when the Neandertal and modern human lineages split suggest that the new form of *FOXP2* must have emerged at least half a million years ago. Most of what distinguishes human language from vocal communication in other species, however, comes not from physical means but cognitive ability, which is often correlated with brain size. Primates generally have a larger brain than would be expected from their body size. But human brain volume has more than tripled since the chimp-human ancestor—a growth spurt that genetics researchers have only begun to unravel.

One of the best-studied examples of a gene linked to brain size in humans and other animals is *ASPM*. Genetic studies of people with a condition known as microcephaly, in which the brain is reduced by up to 70 percent, uncovered the role of *ASPM* and another gene—*CDK5RAP2*—in controlling brain size. More recently, researchers at the University of Chicago, the University of Michigan and the University of Cambridge have shown that *ASPM* experienced several bursts of change over the course of primate evolution, a pattern indicative of positive selection. At least one of these bursts occurred in the human lineage since it diverged from that of chimps and thus was potentially instrumental in the evolution of our large brains.

Other parts of the genome may have influenced the metamorphosis of the human brain less directly. The computer scan that identified HAR1 also found 201 other human accelerated regions, most of which do not encode proteins or even RNA. (A related study conducted at the Wellcome Trust Sanger Institute in Cambridge, England, detected many of the same HARs.) Instead they appear to be regulatory sequences that tell nearby genes when to turn on and off. Amazingly, more than half of the genes located near HARs are involved in brain development and function. And, as is true of *FOXP2,* the products of many of these genes go on to regulate other genes. Thus, even though HARs make up a minute portion of the genome, changes in these regions could have profoundly altered the human brain by influencing the activity of whole networks of genes.

covered by researchers at the University of Oxford, who reported in 2001 that people with mutations in the gene are unable to make certain subtle, high-speed facial movements needed for normal human speech, even though they possess the cognitive ability to process language. The typical human sequence displays several differences from the chimp's: two base substitutions that altered its protein product and many other substitutions that may have led to shifts affecting how, when and where the protein is used in the human body.

GETTY IMAGES (*man and chimp*); GK AND VIKKI HART Getty Images (*chicken*)



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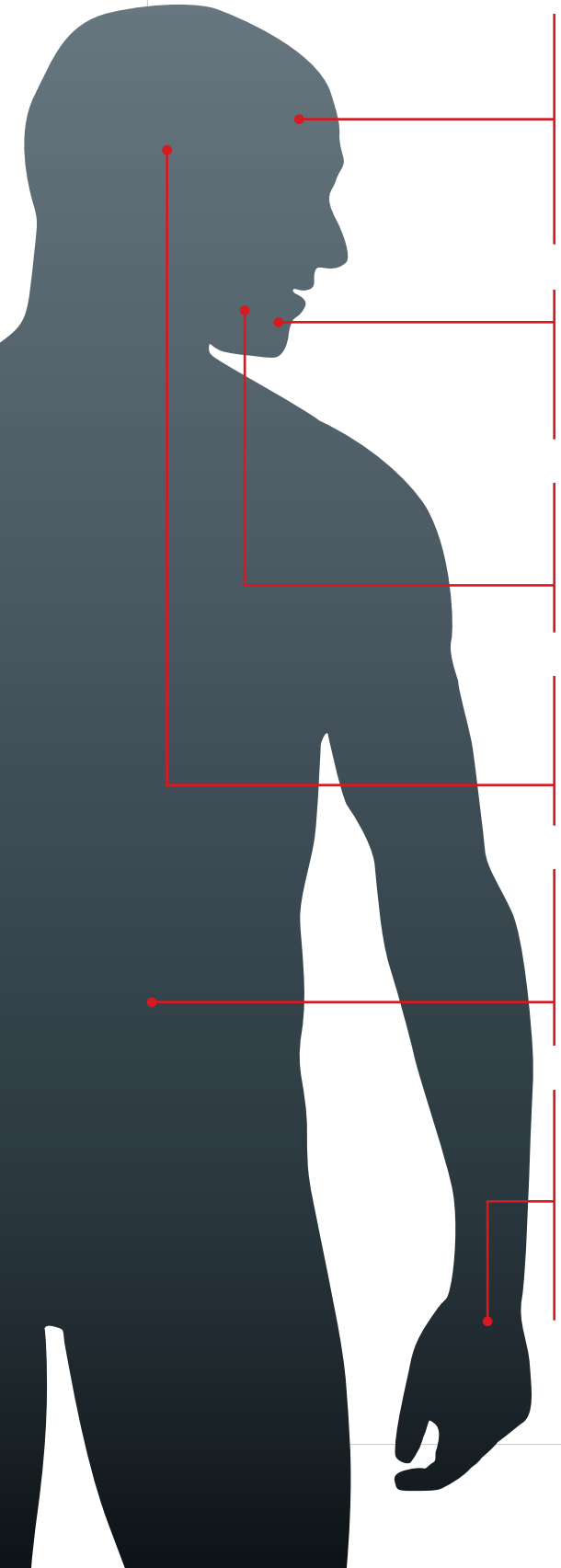
FINDINGS

# Distinctive DNA

**Efforts to uncover** uniquely human DNA have yielded a number of sequences that are distinctive in humans as compared with chimpanzees. A partial list of these sequences—and some of their functions—follows below.



SEQUENCE: HAR1
**WHAT IT DOES:**
Active in the brain; may be necessary for development of the cerebral cortex, which is especially large in humans. Possibly also involved in sperm production.

SEQUENCE: *FOXP2*
**WHAT IT DOES:**
Facilitates formation of words by the mouth, enabling modern human speech.

SEQUENCE: *AMY1*
**WHAT IT DOES:**
Facilitates digestion of starch, which may have enabled early humans to exploit novel foods.

SEQUENCE: *ASPM*
**WHAT IT DOES:**
Controls brain size, which has more than tripled over the course of human evolution.

SEQUENCE: *LCT*
**WHAT IT DOES:**
Permits digestion of milk sugar in adulthood, allowing people to make milk from domesticated animals a dietary staple.

SEQUENCE: HAR2
**WHAT IT DOES:**
Drives gene activity in the wrist and thumb during development, an activity that may have given the hand enough dexterity to make and use complex tools.

MELISSA THOMAS

## BEYOND THE BRAIN

ALTHOUGH MUCH genetic research has focused on elucidating the evolution of our sophisticated brain, investigators have also been piecing together how other unique aspects of the human body came to be. HAR2, a gene regulatory region and the second most accelerated site on my list, is a case in point. In 2008 researchers at Lawrence Berkeley National Laboratory showed that specific base differences in the human version of HAR2 (also known as HACNS1), relative to the version in nonhuman primates, allow this DNA sequence to drive gene activity in the wrist and thumb during fetal development, whereas the ancestral version in other primates cannot. This finding is particularly provocative because it could underpin morphological changes in the human hand that permitted the dexterity needed to manufacture and use complex tools.

Aside from undergoing changes in form, our ancestors also underwent behavioral and physiological shifts that helped them adapt to altered circumstances and migrate into new environments. For example, the conquest of fire more than a million years ago and the agricultural revolution about 10,000 years ago made foods high in starch more accessible. But cultural shifts alone were not sufficient to exploit these calorie-rich comestibles. Our predecessors had to adapt genetically to them.

Changes in the gene *AMY1,* which encodes salivary amylase, an enzyme involved in digesting starch, constitute one well-known adaptation of this kind. The mammalian genome contains multiple copies of this gene, with the number of copies varying between species and even between individual humans. But overall, compared with other primates, humans have an especially large number of *AMY1* copies. In 2007 geneticists at Arizona State University showed that individuals carrying more copies of *AMY1* have more amylase in their saliva, thereby allowing them to digest more starch. The evolution of *AMY1* thus appears to involve both the number of copies of the gene and the specific changes in its DNA sequence.

Another famous example of dietary adaptation involves the gene for lactase (*LCT*), an enzyme that allows mammals to digest the carbohydrate lactose, also known as milk sugar. In most species, only nursing infants can process lactose. But around 9,000 years ago—very recently, in evolutionary terms—changes in the human genome produced versions of *LCT* that allowed adults to digest lactose. Modified *LCT* evolved independently in European and African populations, enabling carriers to digest milk from domesticated animals. Today adult descendants of these ancient herders are much more likely to tolerate lactose in their diets than are adults from other parts of the world,

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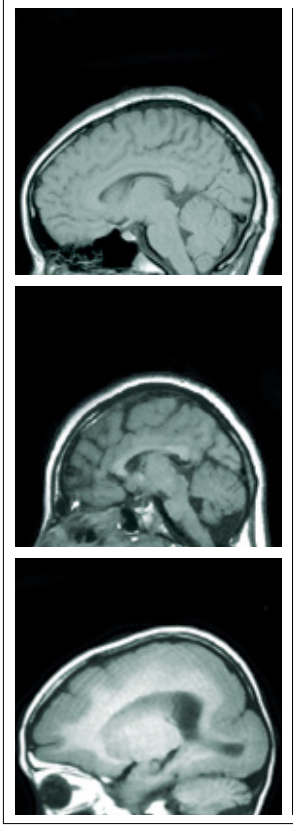
including Asia and Latin America, many of whom are lactose-intolerant as a result of having the ancestral primate version of the gene.

*LCT* is not the only gene known to be evolving in humans right now. The chimp genome project identified 15 others in the process of shifting away from a version that was perfectly normal in our ape ancestors and that works fine in other mammals but, in that old form, is associated with diseases such as Alzheimer's and cancer in modern humans. Several of these disorders afflict humans alone or occur at higher rates in humans than in other primates. Scientists are researching the functions of the genes involved in an attempt to establish why the ancestral versions of these genes became maladaptive in us. These studies could help medical practitioners identify those patients who have a higher chance of getting one of these life-threatening diseases, in hopes of helping them stave off illness. The studies may also help researchers develop new treatments.



**BRAIN SHAPERS:** Changes to certain genome sequences can have dramatic effects on the brain. Mutation of the *ASPM* gene, for example, leads to markedly reduced brain size (*middle*) compared with a normal brain (*top*), suggesting that this gene played a key role in the evolution of large brain size in humans. Malfunctions in the neurons in which HAR1 is active during development, meanwhile, can lead to a severe disorder in which the brain's cerebral cortex fails to fold properly (*bottom*), hinting that HAR1 is essential for the formation of a healthy cortex.

COURTESY OF GANESHWARAN H. MOCHIDA, C. GEOFFREY WOODS AND CHRISTOPHER A. WALSH (*top* and *middle*); COURTESY OF GAVIN UDSTUEN *University of Cincinnati* (*bottom*)

## WITH THE GOOD COMES THE BAD

WHEN RESEARCHERS examine the human genome for evidence of positive selection, the top candidates are frequently involved in immunity. It is not surprising that evolution tinkers so much with these genes: in the absence of antibiotics and vaccines, the most likely obstacle to individuals passing along their genes would probably be a life-threatening infection that strikes before the end of their childbearing years. Further accelerating the evolution of the immune system is the constant adaptation of pathogens to our defenses, leading to an evolutionary arms race between microbes and hosts.

Records of these struggles are left in our DNA. This is particularly true for retroviruses, such as HIV, that survive and propagate by inserting their genetic material into our genomes. Human DNA is littered with copies of these short retroviral genomes, many from viruses that caused diseases millions of years ago and that may no longer circulate. Over time the retroviral sequences accumulate random mutations just as any other sequence does, so that the different copies are similar but not identical. By examining the amount of divergence among these copies, researchers can use molecular clock techniques to date the original retroviral infection. The scars of these ancient infections are also visible in the host immune system genes that constantly adapt to fight the ever evolving retroviruses.

PtERV1 is one such relic virus. In modern humans, a protein called TRIM5α works to prevent PtERV1 and related retroviruses from replicating. Genetic evidence suggests that a PtERV1 epidemic plagued ancient chimps, gorillas and humans living in Africa about four million years ago. To study how different primates responded to PtERV1, in 2007 researchers at the Fred Hutchinson Cancer Research Center in Seattle used the many randomly mutated copies of PtERV1 in the chimp genome to reconstruct the original PtERV1 sequence and recreate this ancient retrovirus. They then performed experiments to see how well the human and great ape versions of the *TRIM5*α gene could restrict the activity of the resurrected PtERV1 virus. Their results indicate that most likely a single change in human *TRIM5*α enabled our ancestors to fight PtERV1 infection more effectively than our primate cousins could.

Defeating one type of retrovirus does not necessarily guarantee continued success against others, however. Even if changes in human *TRIM5*α may have helped us survive PtERV1, these same shifts make it much harder for us to fight HIV. This finding is helping researchers to understand why HIV infection leads to AIDS in humans but less frequently does so in nonhuman primates. Clearly, evolution can take one step forward and two steps back. Sometimes scientific research feels the same way. We have identified many exciting candidates for explaining the genetic basis of distinctive human traits. In most cases, though, we know only the basics about the function of these genome sequences. The gaps in our knowledge are especially large for regions such as HAR1 and HAR2 that do not encode proteins.

These rapidly evolving sequences do point to a way forward. The story of what made us human is probably not going to focus on changes in our protein building blocks but rather on how evolution assembled these blocks in new ways by changing when and where in the body different genes turn on and off. Experimental and computational studies now under way in thousands of labs around the world promise to elucidate what is going on in the 98.5 percent of our genome that does not code for proteins. It is looking less and less like junk every day. SA

### MORE TO EXPLORE


**Mapping Human History: Discovering the Past through Our Genes.** Steve Olson. Houghton Mifflin, 2002.

**The Ancestor's Tale: A Pilgrimage to the Dawn of Evolution.** Richard Dawkins. Houghton Mifflin, 2004.

**Initial Sequence of the Chimpanzee Genome and Comparison with the Human Genome.** Chimpanzee Sequencing and Analysis Consortium in *Nature*, Vol. 437, pages 69–87; September 1, 2005.

University of California, Santa Cruz, Genome Bioinformatics Web site: http://genome.ucsc.edu

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BIOLOGY

# Cooking Up Bigger Brains

Our hominid ancestors probably could not have eaten enough raw food to support large, calorie-hungry brains. The key to our evolution may have been the invention of the kitchen

BY RACHAEL MOELLER GORMAN

RICHARD WRANGHAM HAS TASTED CHIMP FOOD, AND HE DOESN'T LIKE IT. "The typical fruit is very unpleasant," the Harvard University biological anthropologist says of the hard, strangely shaped fruits endemic to the chimp diet, some of which look like cherries, others like cocktail sausages. "Fibrous, quite bitter. Not a tremendous amount of sugar. Some make your stomach heave." After a few tastings in western Uganda, where he works part of the year on his 25-year-old project studying wild chimpanzees, Wrangham came to the conclusion that no human could survive long on such a diet. Besides the unpalatable taste, our weak jaws, tiny teeth and small guts would never be able to chomp and process enough calories from the fruits to support our large bodies.

Then, one cool fall evening in 1997, while gazing into his fireplace in Cambridge, Mass., and contemplating a completely different question—"What stimulated human evolution?"—he remembered the chimp food. "I realized what a ridiculously large difference cooking would make," Wrangham says. Cooking could have made the fibrous fruits, along with the tubers and tough, raw meat that chimps also eat, much more easily digestible, he thought. This innovation could have enabled our chimplike ancestors' gut size to shrink over time; the energy that would have gone to support a larger gut might have instead sparked the evolution of our bigger-brained, larger-bodied, humanlike forebearers.

In the 15 years since coming on his theory, Wrangham has stacked up considerable evidence to support it and even published a book in 2009 entitled *Catching Fire: How Cooking Made Us Human* (Basic Books), yet some archaeologists and anthropologists argue that he is just plain wrong. Wrangham is a chimp researcher, the skeptics point out, not a specialist in human evolution. Most important, they say, archaeological data do not support the use of controlled fire during the period Wrangham's theory requires it to.

**IN BRIEF**

WHO
**RICHARD WRANGHAM**

VOCATION | AVOCATION
**Flame on:** Argues that the practice of cooking food, beginning with *Homo erectus,* ultimately enabled the human brain to evolve to its current large size.

RESEARCH FOCUS
**Into the frying pan:** His theory has many skeptics because only scattered signs of fire use by *H. erectus* exist. One example: a Chinese site where *H. erectus* may have spat hackberry seeds into early campfires (producing spectacular sparks).

BIG PICTURE
**On the importance of the stove:** "Everywhere, everyone expects a cooked meal every evening."

Wrangham, who first encountered chimps as a student of Jane Goodall's in 1970, began his career looking at the way ecological pressures, especially food distribution, affect chimp society. He famously conducted research into chimp violence, leading to his 1996 book *Demonic Males.* But ever since staring into that fire 15 years ago, he has been plagued with thoughts of how humans evolved. "I tend to think about human evolution through the lens of chimps," he remarks. "What would it take to convert a chimpanzeelike ancestor into a human?" Fire to cook food, he reasoned, which led to bigger bodies and brains.

And that is exactly what he found in *Homo erectus,* our ancestor that first appeared 1.6 million to 1.9 million years ago. *H. erectus*'s brain was 50 percent larger than its predecessor's, *Homo habilis,* and it experienced the biggest drop in tooth size in human evolution. "There's no other time that satisfies expectations that we would have for changes in the body that would be accompanied by cooking," Wrangham says.

The problem with his idea: proof is slim that any human could control fire that far back. A 2011 review of European sites found no evidence that early hominins controlled fire until some 300,000 to 400,000 years ago. Consistent signs of cooking came even later, when Neandertals were coping with an ice age. "They developed earth oven cookery," says C. Loring Brace, an emeritus professor of anthropology at the University of Michigan. "And that only goes



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**MODERN HUNTER-GATHERER:** Richard Wrangham

back a couple of hundred thousand years." He and others postulate that the introduction of energy-rich, softer animal products, not cooking, was what led to *H. erectus*'s bigger brain and smaller teeth.

So Wrangham did more research. He examined groups of modern hunter-gatherers all over the world and found that no group currently eats all its food raw. Humans seem to be well adapted to eating cooked food: they need a lot of high-quality calories (brain tissue requires 22 times the energy of skeletal muscle). Wrangham and his colleagues calculated that *H. erectus* (which was in *Homo sapiens*'s size range) would have to eat roughly 12 pounds of raw plants a day, or six pounds of raw plants plus raw meat, to get enough calories to survive.

Studies on modern women show that those on a raw vegetarian diet often miss their menstrual periods because of lack of energy. Adding high-energy raw meat does not help much, either—Wrangham found data showing that even at chimps' chewing rate, which can deliver them 400 food calories per hour, *H. erectus* would have needed to chew raw meat for 5.7 to 6.2 hours a day to fulfill its daily energy needs. When it was not gathering food, it would literally be chewing or digesting that food the rest of the time.

To prove that cooking actually does save energy, in 2011 Wrangham, graduate student Rachel Carmody and their colleague gave experimental mice cooked meat or pounded meat (another processing method) to eat. They found that cooking greatly increased the amount of energy mice obtained from meat, so much that mice eating cooked meat had significantly higher body masses than those eating raw meat, even though caloric intake was the same. Cooked meat provided more energy, perhaps because heat denatures proteins, making them much easier to digest.

Wrangham's theory would fit together nicely if not for that pesky problem of controlled fire. Wrangham points to some promising data: archaeologist Francesco Berna of Boston University recently found solid evidence of controlled fire from one million years ago far inside Wonderwerk Cave in South Africa. And at Koobi Fora in Kenya, anthropologist Ralph Rowlett of the University of Missouri–Columbia has found evidence of scorched earth from 1.5 million years ago that contains a mixture of burned wood types, with no signs of roots having burned underground (a tree struck by lightning would show only one wood type and burned roots).

Still, unless evidence of controlled fire can be regularly confirmed at most *H. erectus* sites, many researchers will remain skeptical of Wrangham's theory. Moreover, other food-based theories can explain the body and brain expansion without flames. One is the expensive tissue hypothesis, put forth in 1995 by Leslie C. Aiello, professor emeritus of biological anthropology at University College London, and physiologist Peter Wheeler of Liverpool John Moores University in England. The main idea of the hypothesis—that smaller guts correlate with bigger brains in primates—fits with Wrangham's theory, but Aiello and Wheeler proposed that energy-dense animal-derived foods, such as soft bone marrow and brain matter, were the reason humans developed these characteristics.

Lacking the proof for widespread fire use by *H. erectus,* Wrangham hopes that DNA data may one day help his cause. "It would be very interesting to compare the human and *H. erectus* genetics data to see when certain characteristics arose, such as when humans evolved improved defenses against Maillard reaction products," he says, referring to the chemical products of cooking certain foods that can lead to carcinogens.

Even without such evidence yet, some think Wrangham's theory is just the thing to shake up the field of human evolution. "You have to listen to what Richard is saying because he has some very interesting, original data," says Aiello, who is also president of the Wenner-Gren Foundation, which supports anthropological research. "Sometimes the most creative ideas come from unexpected places." She points to Goodall, who surprised the world by proving that humans were not the only toolmakers. "It's one of the best illustrations I know of the value of primate research informing our knowledge of human evolution and adaptation," Aiello says.

If Wrangham's strange ideas turn out to be true, we can thank an early hominid counterpart of Jamie Oliver who picked a charred tuber out of a campfire and ate it. Without that person, we might never have been able to examine our origins—or enjoy a good grilled steak—in the first place. SA

**RACHAEL MOELLER GORMAN** is a writer based outside Boston. A Q&A version of her interview with Wrangham is at **www.scientificamerican.com/article.cfm?id=evolving-bigger-brains-th**

YOON S. BYUN Getty Images



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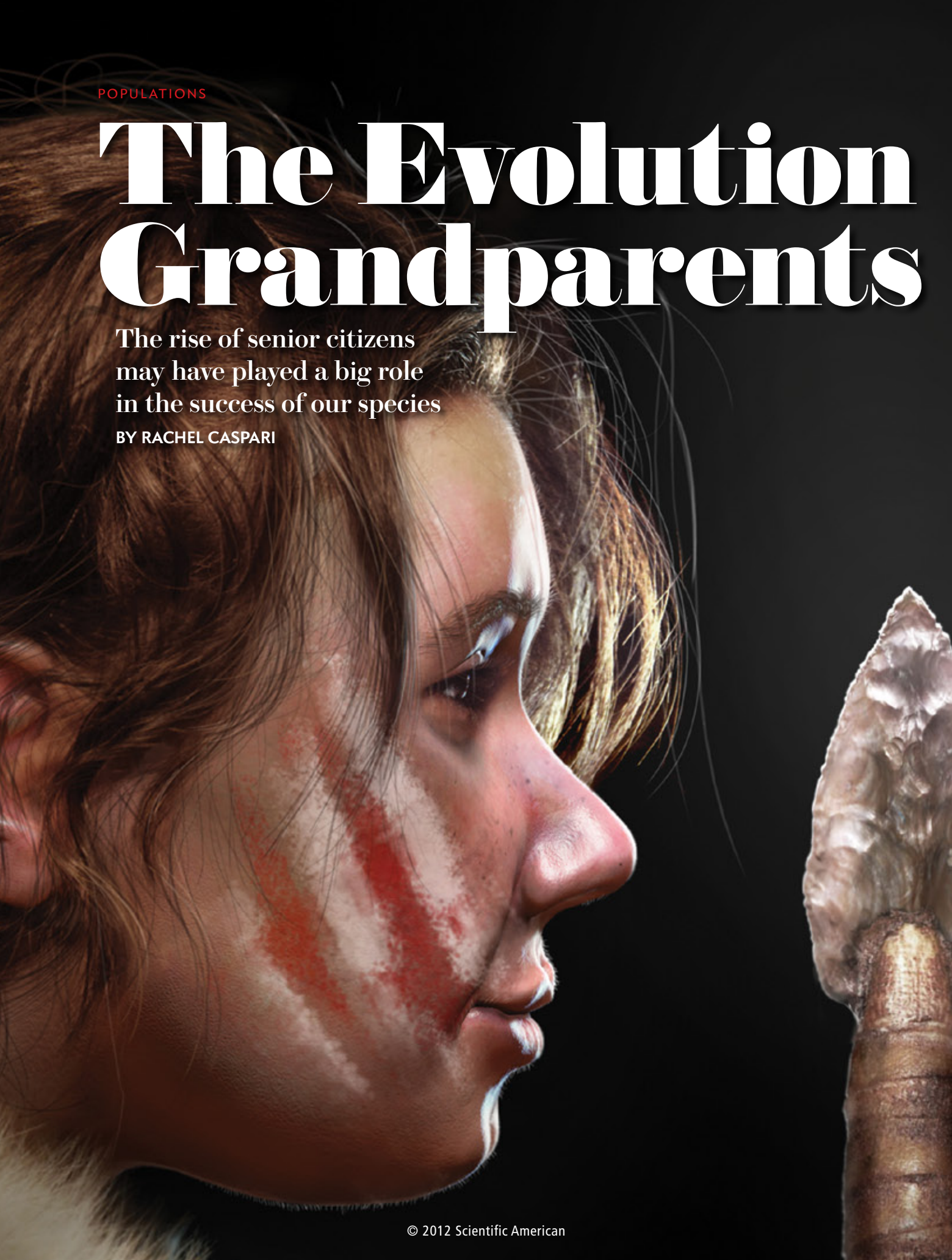
POPULATIONS

# The Evolution of Grandparents

## The rise of senior citizens may have played a big role in the success of our species

BY RACHEL CASPARI



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# of

*Illustration by Viktor Deak*



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DURING THE SUMMER OF 1963, WHEN I WAS SIX YEARS OLD, my family traveled from our home in Philadelphia to Los Angeles to visit my maternal relatives. I already knew my grandmother well: she helped my mother care for my twin brothers, who were only 18 months my junior, and me. When she was not with us, my grandmother lived with her mother, whom I met that summer for the first time. I come from a long-lived family. My grandmother was born in 1895 and her mother in the 1860s; both lived almost 100 years. We stayed with the two matriarchs for several weeks. Through their stories, I learned about my roots and where I belonged in a social network spanning four generations. Their reminiscences personally connected me to life at the end of the Civil War and the Reconstruction era and to the challenges my ancestors faced and the ways they persevered.

My story is not unique. Elders play critical roles in human societies around the globe, conveying wisdom and providing social and economic support for the families of their children and larger kin groups. In our modern era, people routinely live long enough to become grandparents. But this was not always the case. When did grandparents become prevalent, and how did their ubiquity affect human evolution?

Research my colleagues and I have been conducting indicates that grandparent-aged individuals became common relatively recently in human prehistory and that this change came at about the same time as cultural shifts toward distinctly modern behaviors—including a dependence on sophisticated symbol-based communication of the kind that underpins art and language. These findings suggest that living to an older age had profound effects on the population sizes, social interactions and genetics of early modern human groups and may explain why they were more successful than archaic humans, such as the Neandertals.

## LIVE FAST, DIE YOUNG

THE FIRST STEP in figuring out when grandparents became a fixture in society is assessing the typical age breakdown of past populations—what percent were children, adults of childbearing age and parents of those younger adults? Reconstructing the demography of ancient populations is tricky business, however. For one thing, whole populations are never preserved in the fossil record. Rather paleontologists tend to recover fragments of individuals. For another, early humans did not necessarily mature at the same rate as modern humans. In fact, maturation rates differ even among contemporary human populations. But a handful of sites have yielded high enough numbers of human fossils in the same layers of sediment that scientists can confidently assess the age at death of the remains—which is key to understanding the makeup of a prehistoric group.

A rock-shelter located in the town of Krapina in Croatia, about 40 kilometers northwest of the city of Zagreb, is one such site. More than a century ago Croatian paleontologist Dragutin Gorjanović-Kramberger excavated and described the fragmentary remains of perhaps as many as 70 Neandertal individuals there, most of which came from a layer dated to about 130,000 years ago. The large number of fossils found close to one another, the apparently rapid accumulation of the sediments at the site and the fact that some of the remains share distinctive, genetically determined features all indicate that the Krapina bones approximate the remains of a single population of Neandertals. As often happens in the fossil record, the best-preserved remains at Krapina are teeth because the high mineral content of teeth protects them from degradation. Fortunately, teeth are also one of the best skeletal elements for determining age at death, which is achieved by analyzing surface wear and age-related changes in their internal structure.

In 1979, before I began my research into the evolution of grandparents, Milford H. Wolpoff of the University of Michigan published a paper, based on dental remains, that assessed how old the Krapina Neandertals were when they died. Molar teeth erupt sequentially. Using one of the fastest eruption schedules observed in modern-day humans as a guide, Wolpoff estimated that the first, second and third molars of Neandertals erupted at ages that rounded to six, 12 and 15, respectively. Wear from chewing accumulates at a steady pace over an individual's lifetime, so when the second molar emerges, the first already has six years of wear on it, and when the third emerges, the second has three years of wear on it.

Working backward, one can infer, for instance, that a first molar with 15 years of wear on it belonged to a 21-year-old Neandertal, a second molar with 15 years of wear on it belonged to a 27-year-old and a third molar with 15 years of wear on it belonged to a 30-year-old. (These estimates have an uncertainty of plus or minus one year.) This wear-based seriation method for determining age at death, adapted from a technique developed by dental re-

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### IN BRIEF

**People today** typically live long enough to become grandparents, but this was not always the case. **Recent analyses** of fossil teeth indicate that grandparents were rare in ancient populations, such as those of the australopithecines and the Neandertals. They first became common around 30,000 years ago, as evidenced by remains of early modern Europeans. **This surge** in the number of seniors may have been a driving force for the explosion of new tool types and art forms that occurred in Europe at around the same time. It also may explain how modern humans outcompeted archaic groups such as the Neandertals.



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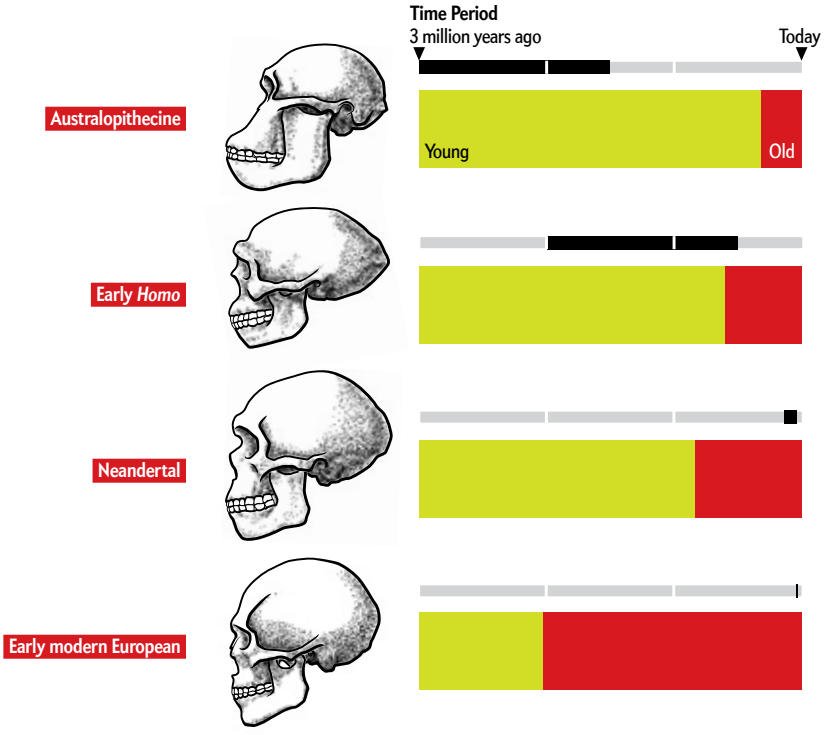
## Growing Older

**Analyses** of the fossilized teeth of hundreds of individuals spanning three million years indicate that living long enough to reach grandparenthood became common relatively late in human evolution. The author and her colleague assessed the proportion of older (grandparent-aged) adults relative to younger adults in four groups of human ancestors—australopithecines, early members of the genus *Homo,* Neandertals and early modern Europeans—and found that the ratio increased only modestly over the course of human evolution until around 30,000 years ago, when it skyrocketed.




searcher A.E.W. Miles in 1963, works best on samples with large numbers of juveniles, which Krapina has in abundance. The method loses accuracy when applied to the teeth of elderly individuals, whose tooth crowns can be too worn to evaluate reliably and in some cases may even be totally eroded.

Wolpoff's work indicated that the Krapina Neandertals died young. In 2005, a few years after I began researching the evolution of longevity, I decided to take another look at this sample using a novel approach. I wanted to make sure that we were not missing older individuals as a result of the inherent limitations of wear-based seriation. With Jakov Radovčić of the Croatian Natural History Museum in Zagreb, Steven A. Goldstein, Jeffrey A. Meganck and Dana L. Begun, then all at Michigan, and undergraduate students from Central Michigan University, I worked to develop a new nondestructive method—using high-resolution three-dimensional microcomputed tomography (μCT)—to reassess how old the Krapina individuals were when they died. Specifically, we looked at the degree of development of a type of tissue within the tooth called secondary dentin; the volume of secondary dentin increases with age and provides a way to assess how old an individual was at death when the tooth crown is too worn to be a good indicator.

Our initial findings, supplemented with scans provided by the Max Planck Institute for Evolutionary Anthropology in Leipzig, corroborated Wolpoff's results and validated the wear-based seriation method: the Krapina Neandertals had remarkably high mortality rates; no one survived past age 30. (This is not to say that Neandertals across the board never lived beyond 30. A few individuals from sites other than Krapina were around 40 when they died.)

By today's standards, the Krapina death pattern is unimaginable. After all, for most people age 30 is the prime of life. And hunter-gatherers lived beyond 30 in the recent past. Yet the Krapina Neandertals are not unique among early humans. The few other human fossil localities with large numbers of individuals preserved, such as the approximately 600,000-year-old Sima de los Huesos site in Atapuerca, Spain, show similar patterns. The Sima de los Huesos people had very high levels of juvenile and young adult mortality, with no one surviving past 35 and very few living even that long. It is possible that catastrophic events or the particular conditions under which the remains became fossilized somehow selected against the preservation of older individuals at these sites. But the broad surveys of the human fossil record—including the material from these unusually rich sites and other sites containing fewer individuals—that my colleagues and I have conducted indicate that dying young was the rule, not the exception. To paraphrase words attributed to British philosopher Thomas Hobbes, prehistoric life really was nasty, brutish and short.

### RISE OF THE GRANDPARENTS

THIS NEW μCT APPROACH has the potential to provide a high-resolution picture of the ages of older individuals in other fossil human populations. But a few years ago, before we hit on this technique, Sang-Hee Lee of the University of California, Riverside, and I were ready to start looking for evidence of changes in longevity over the course of human evolution. We turned to the best approach available at the time: wear-based seriation.

We faced a daunting challenge, though. Most human fossils do not come from sites, such as Krapina, that preserve so many individuals that the remains can be considered reflective of their larger populations. And the smaller the number of contemporaneous individuals found at a site, the more difficult it is to reliably estimate how old members were when they died because of the statistical uncertainties associated with small samples.

But we realized that we could get at the question of when grandparents started becoming common in another way. Instead of

SOURCE: "OLDER AGE BECOMES COMMON LATE IN HUMAN EVOLUTION," BY RACHEL CASPARI AND SANG-HEE LEE, IN *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA*, VOL. 101, NO. 30; JULY 27, 2004

*Illustration by Portia Sloan Rollings, Graphic by Jen Christiansen*



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# Culture Comes of Age

**A marked increase** in adult survivorship starting around 30,000 years ago in Europe may account for the dramatic cultural shift that ensued there as the comparatively simple technology of the Middle Paleolithic gave way to the sophisticated weapons and art of the Upper Paleolithic. Representative artifacts from both cultural traditions are shown here.

Middle Paleolithic
Flint point (*left*) and side scraper (*above*) from Le Moustier, France
Upper Paleolithic
Bone flute from Hohle Fels, Germany
Stone burin from Brassempouy, France
Ceramic Venus figurine from Dolni Vestonice, Czech Republic
ARTIFACTS NOT TO SCALE

asking how long individuals lived, we asked how many of them lived to be old. That is, rather than focusing on absolute ages, we calculated relative ages and asked what proportion of adults survived to the age at which one could first become a grandparent. Our objective was to evaluate changes over evolutionary time in the ratio of older to younger adults—the so-called OY ratio. Among primates, including humans up until very recently, the third molar erupts at about the same time that an individual becomes an adult and reaches reproductive age. Based on data from Neandertals and contemporary hunter-gatherer populations, we inferred that fossil humans got their third molars and had their first child at around age 15. And we considered double that age to mark the beginning of grandparenthood—just as some women today can potentially give birth at age 15 and those women can become grandmothers when their own children reach age 15 and reproduce.

For our purposes, then, any archaic individual judged to be 30 years old or more qualified as an older adult—one old enough to have become a grandparent. But the beauty of the OY ratio approach is that regardless of whether maturation occurred at 10, 15 or 20 years, the number of older and younger individuals in a sample would be unaffected because the start of older adulthood would change accordingly. And because we were only looking to place the fossils in these two broad categories, we could include large numbers of smaller fossil samples in our analysis without worrying about uncertainties in absolute ages.

We calculated the OY ratios for four large aggregates of fossil samples totaling 768 individuals spanning a period of three million years. One aggregate comprised later australopithecines—those primitive relatives of "Lucy," who lived in East Africa and South Africa from three million to 1.5 million years ago. Another aggregate consisted of early members of our genus, *Homo,* from around the globe who lived between two million and 500,000 years ago. The third group was the European Neandertals from 130,000 to 30,000 years ago. And the last consisted of modern Europeans from the early Upper Paleolithic period, who lived between about 30,000 and 20,000 years ago and left behind sophisticated cultural remains.

Although we expected to find increases in longevity over time, we were unprepared for how striking our results would turn out to be. We observed a small trend of increased longevity over time among all samples, but the difference between earlier humans and the modern humans of the Upper Paleolithic was a dramatic fivefold increase in the OY ratio. Thus, for every 10 young adult Neandertals who died between the ages of 15 and 30, there were only four older adults who survived past age 30; in contrast, for every 10 young adults in the European Upper Paleolithic death distribution, there were 20 potential grandparents. Wondering whether the higher numbers of burials at Upper Paleolithic sites might account for the high number of older adults in that sample, we reanalyzed our Upper Paleolithic sample, using only those remains that had not been buried. But we got similar results. The conclusion was inescapable: adult survivorship soared very late in human evolution.

## BIOLOGY OR CULTURE?

NOW THAT LEE AND I had established that the number of potential grandparents surged at some point in the evolution of anatomically modern humans, we had another question on our hands: What

NATURAL HISTORY MUSEUM, LONDON (*flint point and side scraper*); DANITA DELIMONT *Getty Images* (*Venus figurine*); GETTY IMAGES (*flute*); DIDIER DESCOUENS *Museum of Toulouse, France* (*burin*)



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was it that brought about this change? There were two possibilities. Either longevity was one of the constellations of genetically controlled traits that biologically distinguished anatomically modern humans from their predecessors, or it did not come along with the emergence of modern anatomy and was instead the result of a later shift in behavior. Anatomically modern humans did not burst onto the evolutionary scene making the art and advanced weaponry that define Upper Paleolithic culture. They originated long before those Upper Paleolithic Europeans, more than 100,000 years ago, and for most of that time they and their anatomically archaic contemporaries the Neandertals used the same, simpler Middle Paleolithic technology. (Members of both groups appear to have dabbled in making art and sophisticated weapons before the Upper Paleolithic, but these traditions were ephemeral compared with the ubiquitous and enduring ones that characterize that later period.) Although our study indicated that a large increase in grandparents was unique to anatomically modern humans, it alone could not distinguish between the biological explanation and the cultural one, because the modern humans we looked at were both anatomically and behaviorally modern. Could we trace longevity back to earlier anatomically modern humans who were not yet behaviorally modern?

To address this question, Lee and I analyzed Middle Paleolithic humans from sites in western Asia dating to between about 110,000 and 40,000 years ago. Our sample included both Neandertals and modern humans, all associated with the same comparatively simple artifacts. This approach allowed us to compare the OY ratios of two biologically distinct groups (many scholars consider them to be separate species) who lived in the same region and had the same cultural complexity. We found that the Neandertals and modern humans from western Asia had statistically identical OY ratios, ruling out the possibility that a biological shift accounted for the increase in adult survivorship seen in Upper Paleolithic Europeans. Both western Asian groups had roughly even proportions of older and younger adults, putting their OY ratios between those of the Neandertals and early modern humans from Europe.

Compared with European Neandertals, a much larger proportion of western Asian Neandertals (and modern humans) lived to be grandparents. This is not unexpected—the more temperate environment of western Asia would have been far easier to survive in than the harsh ecological conditions of Ice Age Europe. Yet if the more temperate environment of western Asia accounts for the elevated adult survivorship seen in the Middle Paleolithic populations there, the longevity of Upper Paleolithic Europeans is even more impressive. Despite living in much harsher conditions, the Upper Paleolithic Europeans had an OY ratio more than double that of the Middle Paleolithic modern humans.

## SENIOR MOMENTS

WE DO NOT KNOW EXACTLY what those Upper Paleolithic Europeans started doing culturally that allowed so many more of them to live to older age. But there can be no doubt that this increased adult survivorship itself had far-reaching effects. As Kristen Hawkes of the University of Utah, Hillard Kaplan of the University of New Mexico and others have shown in their studies of several modern-day hunter-gatherer groups, grandparents routinely contribute economic and social resources to their descendants, increasing both the number of offspring their children can have and the survivorship of their grandchildren. Grandparents also reinforce complex social connections—like my grandmother did in telling stories of ancestors that linked me to other relatives in my generation.

Elders transmit other kinds of cultural knowledge, too—from environmental (what kinds of plants are poisonous or where to find water during a drought, for example) to technological (how to weave a basket or knap a stone knife, perhaps). Multigenerational families have more members to hammer home important lessons. Thus, longevity presumably fostered the intergenerational accumulation and transfer of information that encouraged the formation of intricate kinship systems and other social networks.

Increases in longevity would also have translated into increases in population size by adding an age group that was not there in the past and that was still fertile. And large populations are major drivers of new behaviors. In 2009 Adam Powell of University College London and his colleagues published a paper in *Science* showing that population density figures importantly in the maintenance of cultural complexity. They and many other researchers argue that larger populations promoted the development of extensive trade networks, complex systems of cooperation, and material expressions of individual and group identity (jewelry, body paint, and so on). Viewed in that light, the hallmark features of the Upper Paleolithic look as though they might well have been consequences of swelling population size.

**Increases in longevity would also have translated into increases in population size by adding an age group that was not there in the past.**

Growing population size would have affected our forebearers another way, too: by accelerating the pace of evolution. As John Hawks of the University of Wisconsin–Madison has emphasized, more people mean more mutations and opportunities for advantageous mutations to sweep through populations as their members reproduce. This trend may have had an even more striking effect on recent humans than on Upper Paleolithic ones, compounding the dramatic population growth that accompanied the domestication of plants 10,000 years ago.

The relation between adult survivorship and the emergence of sophisticated new cultural traditions was almost certainly a positive feedback process. Initially a by-product of some sort of cultural change, longevity became a prerequisite for the complex behaviors that signal modernity. These innovations in turn promoted the importance and survivorship of older adults, which led to the population expansions that had such profound cultural and genetic effects on our predecessors. Older and wiser, indeed. SA

MORE TO EXPLORE

**Older Age Becomes Common Late in Human Evolution.** Rachel Caspari and Sang-Hee Lee in *Proceedings of the National Academy of Sciences USA*, Vol. 101, No. 30, pages 10,895–10,900; July 27, 2004.

**Is Human Longevity a Consequence of Cultural Change or Modern Human Biology?** Rachel Caspari and Sang-Hee Lee in *American Journal of Physical Anthropology*, Vol. 129, pages 512–517; April 2006.



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# Four Fallacies of Pop Evolutionary Psychology

Some evolutionary psychologists have trumpeted claims about how the human mind evolved that other scholars take issue with. Here is how the evidence shapes up

BY DAVID J. BULLER

CHARLES DARWIN WASTED NO TIME APPLYING HIS THEORY OF EVOLUTION TO human psychology, following *On the Origin of Species* (1859) with *The Descent of Man* (1871) and *The Expression of the Emotions in Man and Animals* (1872). Ever since, the issue hasn't been whether evolutionary theory can illuminate the study of psychology but how it will do so. Still, a concerted effort to explain how evolution has affected human behavior began only in the 1970s with the emergence of sociobiology. The core idea of sociobiology was simple: behavior has evolved under natural and sexual selection (in response to competition for survival and reproduction, respectively), just as organic form has. Sociobiology thereby extended the study of adaptation to include human behavior.

**DEFINITION**

As used in this article, pop evolutionary psychology, or Pop EP, refers to a branch of theoretical psychology that employs evolutionary principles to support claims about human nature for popular consumption.

In his 1985 critique of sociobiology, *Vaulting Ambition,* philosopher Philip Kitcher noted that, whereas some sociobiology backed modest claims with careful empirical research, the theoretical reach of the dominant program greatly exceeded its evidential grasp. Kitcher called this program "pop sociobiology" because it employed evolutionary principles "to advance grand claims about human nature and human social institutions" and was "deliberately designed to command popular attention."

Times have changed. Although some self-identified sociobiologists are still around, the current fashion is evolutionary psychology. Evolutionary psychology maintains that adaptation is to be found among the psychological mechanisms that control behavior rather than among behaviors themselves. But, as the old saw goes, the more things change, the more they stay the same. Although some work in evolutionary psychology backs modest claims with careful empirical research, a dominant strain, pop evolutionary psychology, or Pop EP, offers grand and encompassing claims about human nature for popular consumption.

The most notable representatives of Pop EP are psychologists David M. Buss (a professor at the University of Texas at Austin and author of *The Evolution of Desire* and *The Dangerous Passion*) and Steven Pinker (a professor at Harvard University whose



*Photograph by Grant Delin*

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**DIORAMA OF A STONE AGE MAN** as he might have lived some 15,000 years ago was photographed at the Hall of Human Origins at the American Museum of Natural History in New York City.

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books include *How the Mind Works* and *The Blank Slate*). Their popular accounts are built on the pioneering theoretical work of what is sometimes referred to as the Santa Barbara school of evolutionary psychology, led by anthropologists Donald Symons and John Tooby and psychologist Leda Cosmides, all at the University of California, Santa Barbara.

According to Pop EP, "the human brain consists of a large collection of functionally specialized computational devices that evolved to solve the adaptive problems regularly encountered by our hunter-gatherer ancestors" (from the Web site of the Center for Evolutionary Psychology at U.C.S.B.). Just as evolution by natural and sexual selection has endowed all humans with morphological adaptations such as hearts and kidneys, Pop EP says, so it has endowed all humans with a set of psychological adaptations, or "mental organs." These include psychological mechanisms, or "functionally specialized computational devices," for language, face recognition, spatial perception, tool use, mate attraction and retention, parental care and a wide variety of social relations, among other things. Collectively, these psychological adaptations constitute a "universal human nature." Individual and cultural differences are, by this account, the result of our common nature responding to variable local circumstances, much as a computer program's outputs vary as a function of its inputs. The notable exceptions to this rule involve sex differences, which evolved because males and females sometimes faced distinct adaptive problems.

Moreover, because complex adaptation is a very slow process, human nature is designed for the hunter-gatherer lifestyle led by our ancestors in the Pleistocene (the period from 1.8 million to 10,000 years ago). As Cosmides and Tooby colorfully say, "our modern skulls house a Stone Age mind." Pop EP proposes to discover our universal human nature by analyzing the adaptive problems our ancestors faced, hypothesizing the psychological mechanisms that evolved to solve them and then testing those hypotheses using standard-fare psychological evidence, such as pencil-and-paper questionnaires. Pop EP claims that a number of psychological adaptations have been discovered in this way, including evolved sex differences in mate preferences (males prefer nubility;

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**POP EP SAYS**
that we know or can discover why distinctively human traits such as language evolved.

**BUT**
to discover why any trait evolved, we need to identify the adaptive functions it served among early humans, for which we have little evidence.



*Illustrations by Frank Stockton*

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females prefer nobility) and jealousy (men are more distressed by a mate's sexual infidelity, women by emotional infidelity).

I believe that Pop EP is misguided. The ideas suffer not so much from one fundamental flaw as from many small mistakes. Nevertheless, recent critiques of evolutionary psychology point to some general problems of Pop EP.

### FALLACY 1:
### ANALYSIS OF PLEISTOCENE ADAPTIVE PROBLEMS YIELDS CLUES TO THE MIND'S DESIGN

TOOBY AND COSMIDES have argued that because we can be quite certain that our Pleistocene ancestors had to, among other things, "select mates of high reproductive value" and "induce potential mates to choose them," we can also be sure that psychological adaptations evolved for solving these problems. But efforts to identify the adaptive problems that drove human psychological evolution confront a dilemma.

On the one horn, while it is true that our ancestors had to "induce potential mates to choose them," for example, such a description is too abstract to provide any clear indication of the nature of human psychological adaptations. All species face the problem of attracting mates. Male bowerbirds build ornately decorated bowers, male hangingflies offer captured prey, and male sedge warblers sing a wide repertoire of songs. Figuring out which strategies ancestral humans had to use requires a much more precise description of the adaptive problem for early humans.

More precise descriptions of the adaptive problems our ancestors faced, however, get impaled by the other horn of the dilemma: these descriptions are purely speculative because we have little evidence of the conditions under which early human evolution occurred. The paleontological record provides a few clues about some aspects of early human life, but it is largely silent regarding the social interactions that would have been of principal importance in human psychological evolution. Nor do extant hunter-gatherer populations provide many hints about the social lives of our ancestors. Indeed, the lifestyles of these groups vary considerably, even among those who live in the regions of Africa that had been populated by early humans.

Moreover, as biologist Richard Lewontin of Harvard has argued, the adaptive problems faced by a species are not independent of its characteristics and lifestyle. Tree bark contributes to the adaptive problems faced by woodpeckers, but stones lying at the foot of a tree do not. In contrast, for thrushes, which use stones to break snail shells, the stones are part of the adaptive problems they face, whereas tree bark is not. Similarly, our ancestors' motivational and cognitive processes would have been selectively responsive to certain features of the physical and social environments, and this selective responsiveness would have determined which environmental factors affected human evolution. So to identify the adaptive problems that shaped the human mind, we need to know something about ancestral human psychology. But we don't.

Finally, even if we could precisely identify the adaptive problems faced by our ancestors throughout human evolutionary history, we still couldn't infer much about the nature of human psychological adaptations. Selection builds solutions to adaptive problems by retaining modifications to preexisting traits. Subsequent adaptation is always a function of how preexisting traits were modifiable. To know how a solution to an adaptive problem evolved, then, it is necessary to know something about the preexisting trait that was recruited and modified to solve the problem. Without knowledge of our ancestors' psychological traits—which we don't have—we can't know how selection tinkered with them to create the minds we now possess.

**POP EP SAYS**
that analysis of the adaptive problems faced by our Stone Age ancestors, such as how to compete for mates and resources, yields clues to the mind's design.

**BUT**
without knowledge of our ancestors' psychological traits—information we don't have—we can't know how selection tinkered with these traits to create the minds we now have.

**IN BRIEF**

**Among Charles Darwin's** lasting legacies is our knowledge that the human mind evolved by some adaptive process.

**A major, widely discussed** branch of evolutionary psychology—Pop EP—holds that the human brain has many specialized mechanisms that evolved to solve the adaptive problems of our hunter-gatherer ancestors.

**The author and several** other scholars suggest that some assumptions of Pop EP are flawed: that we can know the psychology of our Stone Age ancestors, that we can thereby figure out how distinctively human traits evolved, that our minds have not evolved much since the Stone Age, and that standard psychological questionnaires yield clear evidence of the adaptations.



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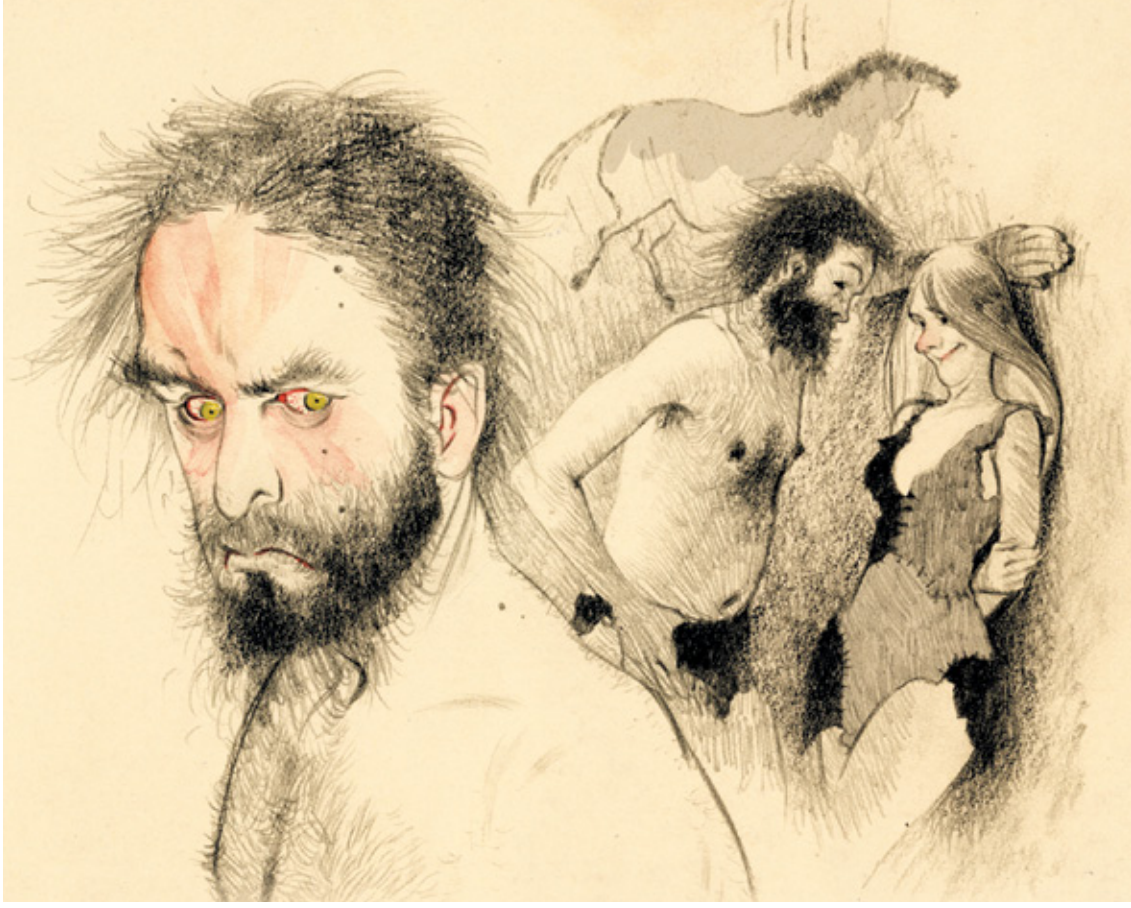
**POP EP SAYS**
that the psychological data provide clear evidence for their claims, such as differences in the basis of jealousy in males and females.

**BUT**
the data are largely based on forced-answer questionnaires [*see box on page 50*]. Such evidence is inconclusive. It gives no clear basis, for example, for thinking that males and females evolved distinct mechanisms of jealousy. Instead both sexes may possess the same mechanism, which simply responds differently when faced with different types of threat to a relationship.



### FALLACY 2: WE KNOW, OR CAN DISCOVER, WHY DISTINCTIVELY HUMAN TRAITS EVOLVED

BIOLOGISTS are often able to reconstruct the selection pressures that drove a species' evolution by using the comparative method to study a clade, or group of species descended from a common ancestor. Because all the species in the group are descended from a common form, differences among them may be the result of variations in the environmental demands they faced. When a trait is shared by two or more species in a clade, but not by the others, it is sometimes possible to identify environmental demands common to those species but absent among the species without the trait. Correlating trait differences with specific environmental variations, in this way, can indicate the environmental demands to which a trait is adapted.

But the comparative method offers little help for Pop EP's aspiration to reveal the adaptive history of the psychological traits—including language and forms of higher cognition—that putatively constitute human nature. Pinker, for example, has argued eloquently that language is an adaptation for verbal communication of infinite combinatorial complexity. He is probably right that language is an adaptation. But discovering why it evolved—what it is an adaptation for—requires identifying the adaptive functions that language served among early language users. To employ the comparative method to answer such questions, we need to compare some human psychological trait with its homologous form in species with whom we share a common ancestor. Here looms the problem. Among extant species, our closest relatives are the chimpanzee and the bonobo, with whom we share a common ancestor that lived approximately six million years ago. But even these, our closest relatives, don't possess forms of the complex psychological traits, such as language, whose evolution Pop EP aspires to explain. So we can't identify the environmental demands we share with our closest relatives to see what our common psychological traits are adapted to. Rather we need to identify the environmental demands that drove our evolutionary separation from our closest living relatives during the past six million years.

What could enlighten us about these evolutionary events would be information about the ecology and lifestyle of more closely related species with whom we share some higher cognitive abilities. Then, perhaps, we could identify environmental demands shared with them but absent among the chimpanzee and the bonobo (and other primates). The species that fit this bill are the other hominins, the australopithecines and the other species in the genus *Homo*. Unfortunately, all other hominins are extinct. And dead hominins tell (virtually) no tales about their evolutionary histories. So there is a dearth of evidence necessary for using the comparative method to illuminate the evolutionary history of distinctively human traits. (That is why there are several theories about the evolution of language but no suggestions about how evidence can be used to choose among them.)

The comparative method does, however, sometimes provide useful information about distinctively human adaptations. But as philosopher Jonathan Michael Kaplan of Oregon State University has pointed out, when it does so, it is not for traits that are universal among humans, but for traits that appear in only some human populations. For example, we know that the gene that produces sickle cell anemia (when a person has two copies of the gene) is an adaptation for resistance to malaria (when a person has just one copy of the gene). Our evidence derived from comparing human populations that have the gene with human populations that don't and identifying the environmental demands correlated with its presence.

Because the comparative method has illuminated such phys-



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iological adaptations, it is reasonable to suppose it could illuminate some psychological adaptations as well. But this is cold comfort to Pop EP, which claims that all human psychological adaptations are, in fact, universal among human populations. It is precisely such universal and distinctively human traits for which the comparative method offers little use. Therefore, it is unlikely that accounts of the evolution of our alleged universal human nature will ever rise above the level of speculation.

### FALLACY 3:
### "OUR MODERN SKULLS HOUSE A STONE AGE MIND"

POP EP'S CLAIM that human nature was designed during the Pleistocene, when our ancestors lived as hunter-gatherers, gets it wrong on both ends of the epoch.

Some human psychological mechanisms undoubtedly did emerge during the Pleistocene. But others are holdovers of a more ancient evolutionary past, aspects of our psychology that are shared with some of our primate relatives. Evolutionary neuroscientist Jaak Panksepp of Bowling Green State University has identified seven emotional systems in humans that originated deeper in our evolutionary past than the Pleistocene. The emotional systems that he terms Care, Panic and Play date back to early primate evolutionary history, whereas the systems of Fear, Rage, Seeking and Lust have even earlier, premammalian origins.

Recognition of our deeper evolutionary history can greatly affect how we understand human psychology. Consider human mating. Buss has argued that human mating strategies were designed during the Pleistocene to solve adaptive problems that were unique in shaping human evolution. Accordingly, observing that humans pursue both short- and long-term mating (sometimes indulging in brief infidelities in the context of an ongoing mateship), he interprets these behaviors as aspects of an integrated set of psychological adaptations that unconsciously calculate the reproductive benefits of each strategy. When the potential reproductive benefits of a short-term mating opportunity are greater than the potential costs, these adaptations lead to infidelity.

If we recognize that aspects of our psychology are holdovers of prehuman evolutionary history, we get a very different picture. Indeed, because our closest relatives, the chimpanzee and bonobo, are highly promiscuous species, our lineage likely embarked on the uniquely human leg of its evolutionary journey with a mechanism of lust designed to promote promiscuous mating. Psychological characteristics that subsequently emerged during human evolutionary history were built atop that foundation. And we know that some emotional systems subsequently evolved to promote the pair bonding that is ubiquitous among human cultures but absent in our closest primate relatives. We have no reason, however, to think that mechanisms of lust and pair bonding evolved together as parts of an integrated mating strategy. Indeed, they likely evolved as separate systems, at diverse points in our lineage's evolutionary history, in response to different adaptive demands, to serve distinct purposes.

**The idea that we are stuck with a Pleistocene-adapted psychology greatly underestimates the rate at which natural and sexual selection can drive evolutionary change.**

If this alternative interpretation of human mating psychology is correct, we are not "of one mind" about our sexual relationships. Instead we possess competing psychological urges. We are pushed toward promiscuity by evolutionarily ancient mechanisms of lust and toward long-term pair bonds by more recently evolved emotional systems. Rather than being driven by an integrated Pleistocene psychology that unconsciously calculates which urge to pursue when, we are torn by independently evolved emotional mechanisms.

The view that "our modern skulls house a Stone Age mind" gets things wrong on the contemporary end of our evolutionary history as well. The idea that we are stuck with a Pleistocene-adapted psychology greatly underestimates the rate at which natural and sexual selection can drive evolutionary change. Recent studies have demonstrated that selection can radically alter the life-history traits of a population in as few as 18 generations (for humans, roughly 450 years).

Of course, such rapid evolution can occur only with significant change in the selection pressures acting on a population. But environmental change since the Pleistocene has unquestionably altered the selection pressures on human psychology. The agricultural and industrial revolutions precipitated fundamental changes in the social structures of human populations, which in turn altered the challenges humans face when acquiring resources, mating, forming alliances or negotiating status hierarchies. Other human activities—ranging from constructing shelter to preserving food, from contraception to organized education—have also consistently altered the selection pressures. Because we have clear examples of post-Pleistocene physiological adaptation to changing environmental demands (such as malaria resistance), we have no reason to doubt similar psychological evolution.

Moreover, human psychological characteristics are the product of a developmental process involving interaction between genes and the environment. Even if little genetic evolution has taken place since the Pleistocene, which is doubtful, human en-

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vironments have changed in profound ways, as the examples above indicate. Any Pleistocene-selected genes we possess will interact with these new environments to produce psychological traits that may differ in important ways from those of our Pleistocene ancestors. So there is no good reason to think that all of our evolved psychological characteristics remain adapted to the lifestyle of Pleistocene hunter-gatherers.

### FALLACY 4: THE PSYCHOLOGICAL DATA PROVIDE CLEAR EVIDENCE FOR POP EP

POP EP ARGUES that its speculations about our Pleistocene past have led to the discovery of many of the psychological adaptations that control our behavior. Because the approach has worked, it must be on to at least part of the truth about human evolutionary history. Of course, the soundness of this argument turns on the strength of the evidence for Pop EP's alleged discoveries. That evidence usually consists of standard psychological pencil-and-paper data (such as responses to forced-choice questionnaires), but it sometimes also includes a limited array of behavioral data. As I argue at length in my book *Adapting Minds,* however, the evidence is typically inconclusive at best. Pop EP's favored evolutionary hypotheses are, as philosopher Robert C. Richardson of the University of Cincinnati has quipped, "speculation disguised as results." The appearance that the evidence is compelling is created less by the data themselves than by the failure to consider and adequately test viable alternative explanations. Consider a single illustration of this point.

Buss argues that jealousy evolved as an emotional alarm that signals a partner's potential infidelities and causes behavior designed to minimize losses of reproductive investment. Among our ancestors, the argument continues, infidelities entailed different reproductive costs for the two sexes. For men, a female's *sexual* infidelity signified that he might be investing parental resources in another male's offspring. For women, it was a male's *emotional* involvement with another woman that could lead to the loss of his resources. And indeed, Buss claims to have discovered the requisite sex difference in the evolved "design features" of the jealous mind: the male mind is more sensitive to cues of sexual infidelity, whereas the female mind is more sensitive to cues of emotional infidelity.

**If cultural variation can result from a common nature responding to dissimilar inputs, surely sex differences in attitudes and behavior can, too.**

The principal data cited in support of this theory are responses to forced-choice questionnaires. One questionnaire item, for example, asks subjects which they find more upsetting: "imagining your partner forming a deep emotional attachment" to a rival or "imagining your partner enjoying passionate sexual intercourse" with a rival. Results consistently show that more men than women report the thought of a partner's sexual infidelity to be more distressing than the thought of a partner's emotional infidelity.

But such data are hardly conclusive evidence of sex-differentiated psychological adaptations. Instead both sexes could have the same evolved capacity to distinguish threatening from nonthreatening infidelities and to experience jealousy to a degree that is proportional to the perceived threat to a relationship in which one has invested mating effort. This shared capacity could generate Buss's questionnaire results because of acquired beliefs about a sex difference in the types of behavior that pose a threat to a relationship. In fact, several studies have found that it is widely believed, by both sexes, that men are more likely than women to have sex in the absence of any emotional involvement. Given this belief, men will

## A Pop EP Questionnaire

To test for an evolved sex difference in jealousy, psychologist David M. Buss and his colleagues designed a questionnaire (*right*), which they administered to American subjects [see "Sex Differences in Jealousy: Evolution, Physiology, and Psychology" in *Psychological Science,* Vol. 3, No. 4; July 1992].

Their questionnaire, or a minor variant of it, was subsequently used in a number of similar studies in several societies. Results of these studies are shown in the tables at the bottom; the first column in each table lists data obtained by Buss and his colleagues in the original study.

**QUESTIONNAIRE**

**Instructions:** Please think of a serious committed romantic relationship that you have had in the past, that you currently have, or that you would like to have. Imagine that you discover that the person with whom you've been seriously involved became interested in someone else. What would distress or upset you more (*circle only one*):

DILEMMA 1

(A) Imagining your partner forming a deep emotional attachment to that person.
(B) Imagining your partner enjoying passionate sexual intercourse with that other person.

DILEMMA 2

(A) Imagining your partner trying different sexual positions with that other person.
(B) Imagining your partner falling in love with that other person.

**SURVEY RESULTS**

Percentage choosing sexual infidelity (B) as more upsetting in Dilemma 1

| | U.S. | U.S. | U.S. | U.S. | U.S. | U.S. | China | Netherlands | Germany | Korea | Japan | Average |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Male | 60 | 76 | 61 | 55 | 53 | 73 | 21 | 51 | 28 | 59 | 38 | 51 |
| Female | 17 | 32 | 18 | 32 | 23 | 4 | 5 | 31 | 16 | 18 | 13 | 22 |

Percentage choosing sexual infidelity (A) as more upsetting in Dilemma 2

| | U.S. | U.S. | U.S. | U.S. | Netherlands | Germany | Korea | Japan | Average |
|---|---|---|---|---|---|---|---|---|---|
| Male | 44 | 43 | 44 | 47 | 23 | 30 | 53 | 32 | 38 |
| Female | 12 | 11 | 12 | 12 | 12 | 8 | 22 | 15 | 13 |



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**POP EP SAYS**
that modern people harbor a Stone Age mind.

**BUT**
it seems just as likely that the human mind had to adapt to dramatic changes brought about by the advent of agriculture and life in cities. Humans have changed physiologically since the Stone Age, so why wouldn't we have changed psychologically as well?

find a woman's sexual infidelity more threatening than women will find a man's sexual infidelity because female sexual infidelity is more likely to be accompanied by emotional involvement.

This alternative hypothesis also readily accounts for data that aren't easily accommodated by the theory that there is a sex difference in the evolved design features of the mind. First, homosexual men are even less likely than heterosexual women to find sexual infidelity more upsetting than emotional infidelity. And homosexual males, as a group, are also less likely than heterosexual males or females to believe that sexual infidelity poses a threat to the primary relationship. If the sexes share the same capacity for jealousy, with the degree of sexual jealousy determined by the degree of the perceived threat to a relationship, homosexual males' tendency not to find sexual infidelity threatening would cause them to depart from the male norm.

Second, the degree to which males find the prospect of a female partner's sexual infidelity upsetting varies significantly among cultures. For example, only about a quarter of German males report sexual infidelity to be more upsetting than emotional infidelity. Interestingly, Buss and his colleagues have themselves noted that the German culture has "more relaxed attitudes about sexuality, including extramarital sex, than does the American culture." So German males should be less likely than American males to believe that a female partner's sexual infidelity threatens a relationship and hence less likely to be distressed by sexual infidelity than American males. Again, this cultural difference is precisely what we should expect if degree of sexual jealousy is a function of the degree to which sexual infidelity is perceived as a threat to a relationship.

It is unclear why Pop EP resists the idea that the sexes share the same emotional mechanism of jealousy and that attitudinal differences are a function of differences in the beliefs processed by the mechanism. According to Pop EP, many cultural differences stem from a common human nature responding to variable local conditions. Yet cultural differences are often more profound than the sex differences that Pop EP has transformed into sensational theory. If cultural variation can result from a common nature responding to dissimilar inputs, surely sex differences in attitudes and behavior can, too.

## CODA

AMONG DARWIN'S lasting legacies is our knowledge that the human mind evolved by some adaptive process. After all, the human brain is even more costly to run than an internal-combustion engine these days, consuming 18 percent of the body's energy intake while constituting merely 2 percent of its weight. We wouldn't have such an organ if it hadn't performed some important adaptive functions in our evolutionary past.

The challenge for evolutionary psychology is to move from this general fact to some evidentially well-supported specifics about the adaptive processes that shaped the mind. Yet, as we have seen, the evidence needed to substantiate accounts of adaptation in our lineage during the past couple of million years is scarce. And this isn't the kind of evidence that is likely to materialize; such evidence is lost to us, probably forever. It may be a cold, hard fact that there are many things about the evolution of the human mind that we will never know and about which we can only idly speculate.

Of course, some speculations are worse than others. Those of Pop EP are deeply flawed. We are unlikely ever to learn much about our evolutionary past by slicing our Pleistocene history into discrete adaptive problems, supposing the mind to be partitioned into discrete solutions to those problems, and then supporting those suppositions with pencil-and-paper data. The field of evolutionary psychology will have to do better. Even its very best, however, may never provide us knowledge of why all our complex human psychological characteristics evolved. SA

### MORE TO EXPLORE


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**CAVE** today known simply as PP13B, near Mossel Bay, South Africa, sheltered humans between 164,000 and 35,000 years ago, at a time when *Homo sapiens* was in danger of dying out. These people may have been the ancestors of us all.



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PALEOCLIMATE

# When the Sea Saved Humanity

Shortly after *Homo sapiens* arose, harsh climate conditions nearly extinguished our species. Recent finds suggest that the small population that gave rise to all humans alive today survived by exploiting a unique combination of resources along the southern coast of Africa

BY CURTIS W. MAREAN

With the global population of humans currently approaching seven billion, it is difficult to imagine that *Homo sapiens* was once an endangered species. Yet studies of the DNA of modern-day people indicate that, once upon a time, our ancestors did in fact undergo a dramatic population decline. Although scientists lack a precise timeline for the origin and near extinction of our species, we can surmise from the fossil record that our forebearers arose throughout Africa before the beginning of the glacial period. Back then the climate was mild and food was plentiful; life was good. But around 195,000 years ago, conditions began to deteriorate. The planet entered a long glacial stage known as Marine Isotope Stage 6 (MIS6) that lasted until roughly 123,000 years ago.

A detailed record of Africa's environmental conditions during glacial stage 6 does not exist, but based on more recent, better-known glacial stages, climatologists surmise that it was almost certainly cool and arid and that its deserts were probably significantly expanded relative to their modern extents. Much of the landmass would have been uninhabitable. While the planet was in the grip of this icy regime, the number of people plummeted

IN BRIEF

**At some point** between 195,000 and 123,000 years ago, the population size of *Homo sapiens* plummeted, thanks to cold, dry climate conditions that left much of our ancestors' African homeland uninhabitable. **Everyone alive today** is descended from a group of people from a single region who survived this catastrophe. The southern coast of Africa would have been one of the few spots where humans could survive during this climate crisis because it harbors an abundance of shellfish and edible plants. **Excavations of a series** of sites in this region have recovered items left behind by what may have been that progenitor population. **The discoveries confirm** the idea that advanced cognitive abilities evolved earlier than previously thought—and may have played a key role in the survival of the species during tough times.

*Illustration by Jean-Francois Podevin*



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perilously—from more than 10,000 breeding individuals to just hundreds. Estimates of exactly when this bottleneck occurred and how small the population became vary among genetic studies, but all of them indicate that everyone alive today is descended from a small population that lived in one region of Africa sometime during this global cooling phase.

I began my career as an archaeologist working in East Africa and studying the origin of modern humans. But my interests began to shift when I learned of the population bottleneck that geneticists had started talking about in the early 1990s. Humans today exhibit very low genetic diversity relative to many other species with much smaller population sizes and geographical ranges—a phenomenon that is best explained by the occurrence of a population crash in early *H. sapiens*. Where, I wondered, did our ancestors manage to survive during the climate catastrophe? Only a handful of regions could have had the natural resources to support groups of hunter-gatherers. Paleoanthropologists argue vociferously over which of these areas was the ideal spot. The southern coast of Africa, rich in shellfish and edible plants year-round, seemed to me as if it would have been a particularly good refuge in tough times. So, in 1991, I decided I would go there and look for sites with remains dating to glacial stage 6.

My search within that coastal area was not random. I had to find a shelter close enough to the ancient coastline to provide easy access to shellfish and elevated enough that its archaeological deposits would not have been washed away 123,000 years ago when the climate warmed and sea levels surged. In 1999 my South African colleague Peter Nilssen and I decided to investigate some caves he had spotted at a place called Pinnacle Point, a promontory near the town of Mossel Bay that juts into the Indian Ocean. Scrambling down the sheer cliff face, we came across a cave that looked particularly promising—one known simply as PP13B. Erosion of the sedimentary deposits located near the mouth of the cave had exposed clear layers of archaeological remains, including hearths and stone tools. Even better, a sand dune and a layer of stalagmite capped these remnants of human activity, suggesting that they were quite old. By all appearances, we had hit the jackpot. The following year, after a local ostrich farmer built us a 180-step wooden staircase to allow safer access to the site, we began to dig.

Since then, my team's excavations at PP13B and other nearby sites have recovered a remarkable record of the activities undertaken by the people who inhabited this area between approximately 164,000 and 35,000 years ago, hence during the bottleneck and after the population began to recover. The deposits in these caves, combined with analyses of the ancient environment there, have enabled us to piece together a plausible account of how the prehistoric residents of Pinnacle Point eked out a living during a grim climate crisis. The remains also debunk the abiding notion that cognitive modernity evolved long after anatomical modernity: evidence of behavioral sophistication abounds in even the oldest archaeological levels at PP13B. This advanced intellect no doubt contributed significantly to the survival of the species, enabling our forebearers to take advantage of the resources available on the coast.

While elsewhere on the continent populations of *H. sapiens* died out as cold and drought claimed the animals and plants they hunted and gathered, the lucky denizens of Pinnacle Point were feasting on the seafood and carbohydrate-rich plants that proliferated there despite the hostile climate. As glacial stage 6 cycled through its relatively warmer and colder phases, the seas rose and fell, and the ancient coastline advanced and retreated. But so long as people tracked the shore, they had access to an enviable bounty.

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## A COASTAL CORNUCOPIA

FROM A SURVIVAL STANDPOINT, what makes the southern edge of Africa attractive is its unique combination of plants and animals. There a thin strip of land containing the highest diversity of flora for its size in the world hugs the shoreline. Known as the Cape Floral Region, this 90,000-square-kilometer strip contains an astonishing 9,000 plant species, some 64 percent of which live only there. Indeed, the famous Table Mountain that rises above Cape Town in the

PER-ANDERS PETTERSSON (*cave sites*); DON FOLEY (*map*); LUCY READING-IKKANDA (*globe*)

**HIGH AND DRY: Finding archaeological sites dating to glacial stage 6 required searching for shelters that were close enough to the sea to allow relatively easy access to shellfish yet elevated enough that their ancient remains would not have washed away when the sea level rose 123,000 years ago. PP13B and other caves carved into the sheer cliff face of a promontory called Pinnacle Point meet those requirements and have yielded a plethora of remains dating to this critical juncture in human prehistory.**



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**SEASIDE SANCTUARY:** Between 195,000 and 123,000 years ago the planet was locked in an ice age known as Marine Isotope Stage 6, rendering much of the African continent cool and arid—unsuitable for the plants and animals that *H. sapiens* ate. Only a few regions could have supported our species, namely, those with grassland or Mediterranean scrub vegetation. The southern coast would have been a particularly plentiful oasis, thanks to the edible fynbos plants that grow only there and the dense shellfish beds nurtured by the Agulhas current and the Benguela upwelling of nutrient-rich cold water from the sea bottom.



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**GONE SHELLFISHING: Shellfish, which are rich in protein, are thought to have aided survival of the Pinnacle Point population because they abound year-round in the rocky intertidal zone along the southern coast of Africa (*upper left*). Brown mussels (*lower left*) have turned up in even the earliest levels of PP13B, dating to 164,000 years ago, revealing that humans began exploiting marine resources earlier than previously thought. In addition to mussels, the occupants of the Pinnacle Point sites collected various kinds of limpets as well as sea snails called alikreukel for food and gathered empty shells of helmet snails for their aesthetic appeal (*above*).**

heart of the Cape Floral Region has more species of plants than does the entire U.K. Of the vegetation groups that occur in this realm, the two most extensive are the fynbos and the renosterveld, which consist largely of shrubs. To a human forager equipped with a digging stick, they offer a valuable commodity: the plants in these groups produce the world's greatest diversity of geophytes—underground energy-storage organs such as tubers, bulbs and corms.

Geophytes are an important food source for modern-day hunter-gatherers for several reasons. They contain high amounts of carbohydrate; they attain their peak carbohydrate content reliably at certain times of year; and, unlike aboveground fruits, nuts and seeds, they have few predators. The bulbs and corms that dominate the Cape Floral Region are additionally appealing because in contrast to the many geophytes that are highly fibrous, they are low in fiber relative to the amount of energy-rich carbohydrate they contain, making them more easily digested by children. (Cooking further enhances their digestibility.) And because geophytes are adaptations to dry conditions, they would have been readily available during arid glacial phases.

The southern coast also has an excellent source of protein to offer, despite not being a prime hunting ground for large mammals. Just offshore, the collision of nutrient-rich cold waters from the Benguela upwelling and the warm Agulhas current creates a mix of cold and warm eddies along the southern coast. This varied ocean environment nurtures diverse and dense beds of shellfish in the rocky intertidal zones and sandy beaches. Shellfish are a very high quality source of protein and omega-3 fatty acids. And as with geophytes, glacial cooling does not depress their numbers. Rather, lower ocean temperatures result in a greater abundance of shellfish.

## SURVIVAL SKILLS

WITH ITS COMBINATION of calorically dense, nutrient-rich protein from the shellfish and low-fiber, energy-laden carbs from the geophytes, the southern coast would have provided an ideal diet for early modern humans during glacial stage 6. Furthermore, women could obtain both these resources on their own, freeing them from relying on men to provision them and their children with high-quality food. We have yet to unearth proof that the occupants of PP13B were eating geophytes—sites this old rarely preserve organic remains—although younger sites in the area contain exten-

PER-ANDERS PETTERSSON



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sive evidence of geophyte consumption. But we have found clear evidence that they were dining on shellfish. Studies of the shells found at the site conducted by Antonieta Jerardino of the University of Barcelona show that people were gathering brown mussels and local sea snails called alikreukel from the seashore. They also ate marine mammals such as seals and whales on occasion.

Previously the oldest known examples of humans systematically using marine resources dated to less than 120,000 years ago. But dating analyses performed by Miryam Bar-Matthews of the Geological Survey of Israel and Zenobia Jacobs of the University of Wollongong in Australia have revealed that the PP13B people lived off the sea far earlier than that: as we reported in 2007 in the journal *Nature,* marine foraging there dates back to a stunning 164,000 years ago. By 110,000 years ago the menu had expanded to include species such as limpets and sand mussels.

This kind of foraging is harder than it might seem. The mussels, limpets and sea snails live on the rocks in the treacherous intertidal zone, where an incoming swell could easily knock over a hapless collector. Along the southern coast, safe harvesting with sufficiently high returns is only possible during low spring tides, when the sun and moon align, exerting their maximum gravitational force on the ebb and flow of the water. Because the tides are linked to the phases of the moon, advancing by 50 minutes a day, I surmise that the people who lived at PP13B—which 164,000 years ago was located much farther inland, two to five kilometers from the water, because of lower sea levels—scheduled their trips to the shore using a lunar calendar of sorts, just as modern coastal people have done for ages.

**DIGGING FOR DINNER:** **Geophytes, the underground energy-storage organs of certain kinds of plants (*left*), swell with edible carbohydrates at certain times of the year. The distinctive vegetation that hugs the southern coast of Africa, particularly the fynbos plants (*right*), produces especially nutritious and easily digested geophytes, which presumably served as a staple for the early modern humans who lived in this region during glacial stage 6.**

Harvesting shellfish is not the only advanced behavior in evidence at Pinnacle Point as early as 164,000 years ago. Among the stone tools are significant numbers of "bladelets"—tiny flakes twice as long as they are wide—that are too small to wield by hand. Instead they must have been attached to shafts of wood and used as projectile weapons. Composite toolmaking is indicative of considerable technological know-how, and the bladelets at PP13B are among the oldest examples of it. But we soon learned that these tiny implements were even more complex than we thought.

Most of the stone tools found at coastal South African archaeological sites are made from a type of stone called quartzite. This coarse-grained rock is great for making large flakes, but it is difficult to shape into small, refined tools. To manufacture the bladelets, people used fine-grained rock called silcrete. There was something odd about the archaeological silcrete, though, as observed by Kyle S. Brown, now at the University of Cape Town, an expert stone tool flaker on my team. After years of collecting silcrete from all over the coast, Brown determined that in its raw form the rock never has the lustrous red and gray coloring seen in the silcrete implements at Pinnacle Point and elsewhere. Furthermore, the raw silcrete is virtually impossible to shape into bladelets. Where, we wondered, did the toolmakers find their superior silcrete?

A possible answer to this question came from Pinnacle Point Cave 5-6, where one day in 2008 we found a large piece of silcrete embedded in ash. It had the same color and luster seen in the silcrete found at other archaeological deposits in the region. Given the association of the stone with the ash, we asked ourselves whether the ancient toolmakers might have exposed the silcrete to fire to make it easier to work with—a strategy that has been documented in ethnographic accounts of native North Americans and Australians. To find out, Brown carefully "cooked" some raw silcrete and then attempted to knap it. It flaked wonderfully, and the flaked surfaces shone with the same luster seen in the artifacts from our sites. We thus concluded that the Stone Age silcrete was also heat-treated.

We faced an uphill battle to convince our colleagues of this remarkable claim, however. It was archaeology gospel that the Solutrean people in France invented heat treatment about 20,000 years ago, using it to make their beautiful tools. To bolster our case, we used three independent techniques. Chantal Tribolo of the University of Bordeaux performed what is called thermoluminescence analysis to determine whether the silcrete tools from Pinnacle Point were intentionally heated. Then Andy Herries of the University of New South Wales in Australia employed magnetic susceptibility, which looks for changes in the ability of rock to be magnetized—another indicator of heat exposure among iron-rich rocks. Finally, Brown used a gloss meter to measure the luster that develops after heating and flaking and compare it with the luster on the tools he made. Our results, detailed in 2009 in the journal *Science,* showed that intentional heat treatment was a dominant technology at Pinnacle Point by 72,000 years ago and that people there employed it intermittently as far back as 164,000 years ago.

The process of treating by heat testifies to two uniquely modern human cognitive abilities. First, people recognized that they could substantially alter a raw material to make it useful—in this case, engineering the properties of stone by heating it, thereby turning a poor-quality rock into high-quality raw material. Second, they could invent and execute a long chain of processes. The making of silcrete blades requires a complex series of carefully designed steps: building a sand pit to insulate the silcrete, bringing the heat slowly up to 350 degrees Celsius, holding the temperature steady and then dropping it down slowly. Creating and carrying out the sequence and passing technologies down from generation to generation probably required language. Once established, these abilities no doubt helped our ancestors outcompete the archaic human species they encountered once they dispersed from Africa. In particular, the complex pyrotechnology detected at Pinnacle Point would have given early modern humans a distinct advan-

COURTESY OF J. C. DE VYNCK



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**PROBING THE PAST:** Continued excavation of PP5-6 and other caves along the southern coast of Africa should reveal more about the progenitor population of humans who survived the bottleneck and colonized the globe.

PER-ANDERS PETTERSSON

tage as they entered the cold lands of the Neandertals, who seem to have lacked this technique.

## SMART FROM THE START

IN ADDITION to being technologically savvy, the prehistoric denizens of Pinnacle Point had an artistic side. In the oldest layers of the PP13B sequence, my team has unearthed dozens of pieces of red ochre (iron oxide) that were variously carved and ground to create a fine powder that was probably mixed with a binder such as animal fat to make paint that could be applied to the body or other surfaces. Such decorations typically encode information about social identity or other important aspects of culture—that is, they are symbolic. Many of my colleagues and I think that this ochre constitutes the earliest unequivocal example of symbolic behavior on record and pushes the origin of such practices back by tens of thousands of years. Evidence of symbolic activities also appears later in the sequence. Deposits dating to around 110,000 years ago include both red ochre and seashells that were clearly collected for their aesthetic appeal because by the time they washed ashore from their deepwater home, any flesh would have been long gone. I think these decorative seashells, along with the evidence for marine foraging, signal that people had, for the first time, begun to embed in their worldview and rituals a clear commitment to the sea.

The precocious expressions of both symbolism and sophisticated technology at Pinnacle Point have major implications for understanding the origin of our species. Fossils from Ethiopia show that anatomically modern humans had evolved by at least 195,000 years ago. The emergence of the modern mind, however, is more difficult to establish. Paleoanthropologists use various proxies in the archaeological record to try to identify the presence and scope of cognitive modernity. Artifacts made using technologies that require outside-the-box connections of seemingly unrelated phenomena and long chains of production—like heat treatment of rock for tool manufacture—are one proxy. Evidence of art or other symbolic activities is another, as is the tracking of time through proxies such as lunar phases. For years the earliest examples of these behaviors were all found in Europe and dated to after 40,000 years ago. Based on that record, researchers concluded that there was a long lag between the origin of our species and the emergence of our peerless creativity.

But over the past decade or so archaeologists working at a number of sites in South Africa have found examples of sophisticated behaviors that predate by a long shot their counterparts in Europe. For instance, archaeologist Ian Watts, who works in South Africa, has described hundreds to thousands of pieces of worked and unworked ochre at sites dating as far back as 120,000 years ago. Interestingly, this ochre, as well as the pieces at Pinnacle Point, tends to be red despite the fact that local sources of the mineral exhibit a range of hues, suggesting that humans were preferentially curating the red pieces—perhaps associating the color with menstruation and fertility. Jocelyn A. Bernatchez, a Ph.D. student at Arizona State University, thinks that many of these ochre pieces may have been yellow originally and then heat-treated to turn them red. And at Blombos Cave, located about 100 kilometers west of Pinnacle Point, Christopher S. Henshilwood of the University of Bergen in Norway has discovered pieces of ochre with systematic engravings, beads made of snail shells and refined bone tools, all of which date to around 71,000 years ago.

These sites, along with those at Pinnacle Point, belie the claim that modern cognition evolved late in our lineage and suggest



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instead that our species had this faculty at its inception.

I suspect that a driving force in the evolution of this complex cognition was strong long-term selection acting to enhance our ancestors' ability to mentally map the location and seasonal variation of many species of plants in arid environments and to convey this accumulated knowledge to offspring and other group members. This capacity laid the foundation for many other advances, such as the ability to grasp the link between the phases of the moon and the tides and to learn to schedule their shellfish-hunting trips to the shore accordingly. Together the readily available shellfish and geophytes provided a high-quality diet that allowed people to become less nomadic, increased their birth rates and reduced their child mortality. The larger group sizes that resulted from these changes would have promoted symbolic behavior and technological complexity as people endeavored to express their social identity and build on one another's technologies, explaining why we see such sophisticated practices at PP13B.

**CUTTING-EDGE TECHNOLOGY:** **Stone tools found in PP5-6 include sophisticated implements such as microblades (*bottom two rows*), which would have been attached to a wooden shaft to form projectile weapons. The toolmakers also appear to have heat-treated the stone to make it easier to shape—a technique that was believed to have originated much later and in France.**

## FOLLOW THE SEA

PP13B PRESERVES a long record of changing occupations that, in combination with the detailed records of local climate and environmental change my team has obtained, is revealing how our ancestors used the cave and the coast over millennia. Modeling the paleocoastline over time, Erich C. Fisher, now at Arizona State, has shown that the conditions changed quickly and dramatically, thanks to a long, wide, gently sloping continental shelf off the coast of South Africa called the Agulhas bank. During glacial periods, when sea levels fell, significant amounts of this shelf would have been exposed, putting considerable distance—up to 95 kilometers—between Pinnacle Point and the ocean. When the climate warmed and sea levels rose, the water advanced over the Agulhas bank again, and the caves were seaside once more.

Judging from rainfall and vegetation patterns evident in records from stalagmites—spanning the time between 350,000 and 50,000 years ago—and in Fisher's paleoscape model, I think that a geophyte-rich plain was revealed as the coast retreated, keeping the geophytes and shellfish in close proximity. I also think that large mammals migrated across that plain, providing the occupants with a third rich source of food to add to the geophytes and shellfish. As for the people, during these periods of low population density they were free to target the best part of the landscape, which was the intersection of the geophytes and shellfish—so I suspect they followed the sea. The tracking of resources would explain why PP13B appears to have been occupied intermittently.

Our excavations at PP13B have intercepted the people who may very well be the ancestors of everyone on the planet as they shadowed the shifting shoreline. Yet if I am correct about these people and their connection to the coast, the richest record of the progenitor population lies underwater on the Agulhas bank. There it will remain for the near future, guarded by great white sharks and dangerous currents. We can still test the hypothesis that humans followed the sea by examining sites on the current coast such as PP13B and another site we are excavating called PP5-6. But we can also study locations where the continental shelf drops steeply and the coast was always near—investigations that my colleagues and I are now initiating.

The genetic, fossil and archaeological records are reasonably concordant in suggesting that the first substantial and prolonged wave of modern human migration out of Africa occurred around 50,000 years ago. Questions about the events leading up to that exodus remain. We do not know whether at the end of glacial stage 6 there was just one population of *H. sapiens* left in Africa or whether there were several, with one ultimately giving rise to everyone alive today. Such unknowns are providing my team and others with a very clear research direction for the foreseeable future: our fieldwork needs to target the other potential progenitor zones in Africa during that glacial period and expand our knowledge of the climate conditions just before that stage. We need to flesh out the story of these people who eventually pushed out of their refuge, filled up the African continent and went on to conquer the world. SA

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See an interactive presentation at www.scientificamerican.com/article.cfm?id=interactive-seas-saved-humanity

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GENETICS

# Traces of a Distant Past

DNA furnishes an ever clearer picture of the multimillennial trek from Africa all the way to the tip of South America

BY GARY STIX

IN BRIEF

**Scientists** trace the path of human migrations by using bones, artifacts and DNA. Ancient objects, however, are hard to find.

**DNA** from contemporary humans can be compared to determine how long an indigenous population has lived in a region.

**The latest studies** survey swaths of entire genomes and produce maps of human movements. They describe how genes have adapted to changes in diet, climate and disease.

SOURCES: DANIEL SAMBRAUS (*human skull*), PASCAL GOETGHELUCK (*Neanderta l skull*), BIOPHOTO ASSOCIATES *Photo Researchers, Inc. (chromosomes)*



*Illustration by Sean McCabe*

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A DEVELOPMENT COMPANY CONTROLLED BY OSAMA BIN LADEN'S HALF BROTHER ONCE ADVANCED the idea that it wanted to build a bridge that would span the Bab el Mandeb, the outlet of the Red Sea to the Indian Ocean. If this ambitious project is ever realized, the throngs of African pilgrims who traverse one of the longest bridges in the world on a journey to Mecca will pass hundreds of feet above the route of the most memorable journey in human history. Fifty or sixty thousand years ago a small band of Africans—a few hundred or even several thousand—may have crossed the strait in tiny boats, never to return. That is just one theory for how modern humans first left Africa. An alternative explanation to a journey over water has these sojourners moving up the coast and through the Sinai Peninsula.

Whether the exit route was over water or land, the reason these travelers left their homeland in eastern Africa is not completely understood. Perhaps the climate changed, or once abundant shellfish stocks vanished. But some things are fairly certain. Those first trekkers out of Africa brought with them the physical and behavioral traits—the large brains and the capacity for language—that characterize fully modern humans. From their bivouac on the Asian continent in what is now Yemen, they appear to have set out on a decamillennial journey that spanned continents and land bridges and reached all the way to Tierra del Fuego, at the bottom of South America.

Scientists, of course, have gained insight into these wanderings because of the fossilized bones or spearheads laboriously uncovered and stored in collections. But ancestral hand-me-downs are often too scant to provide a complete picture of this remote history. In the past 25 years population geneticists have begun to fill in gaps in the paleoanthropological record by fashioning a genetic bread-crumb trail of the earliest migrations by modern humans.

Almost all our DNA—99.9 percent of the three billion "letters," or nucleotides, that make up the human genome—is the same from person to person. But interwoven in that last 0.1 percent are telltale differences. A comparison among, say, East Africans and Native Americans can yield vital clues to human ancestry and to the inexorable progression of colonizations from continent to continent. Until recent years, DNA passed down only from fathers to sons or from mothers to their children has served as the equivalent of fossilized footprints for geneticists. The newest research lets scientists adjust their focus, widening the field of view beyond a few isolated stretches of DNA to inspect hundreds of thousands of nucleotides scattered throughout the whole genome.

Scanning broadly has produced global migratory maps of unprecedented resolution, some of which have been published only during recent years. The research provides an endorsement of modern human origins in Africa and shows how that continent served as a reservoir of genetic diversity that trickled out to the rest of the world. A genetic family tree that begins with the San people of Africa at its root ends with South American Indians and with Pacific Islanders on its youngest-growing branches.

The study of human genetic variation—a kind of historical Global Positioning System—goes back to World War I, when two physicians working in the Greek city of Thessaloníki found that soldiers garrisoned there had a differing incidence of a given blood group depending on their nationality. Beginning in the 1950s, Luigi Luca Cavalli-Sforza started formalizing the study of genetic differences among populations by examining distinct blood group proteins. Variations in proteins reflect differences in the genes that encode them.

Then, in 1987, Rebecca L. Cann and Allan C. Wilson, then at the University of California, Berkeley, published a groundbreaking paper based on analyzing the DNA of mitochondria, the cell's energy-producing organelles, which are passed down through the maternal line. They reported that humans from different populations all descended from a single female in Africa who lived about 200,000 years ago—a finding that immediately made headlines trumpeting the discovery of the "Mitochondrial Eve." (Despite the Biblical allusion, this Eve was not the first woman: her lineage, though, is all that has survived.)

## HITCHHIKING

Microorganisms that ride in or on people can help researchers confirm discoveries about human migrations. The genes of *Helicobacter pylori* (*above*), the ulcer-causing bacterium endemic to humans, indicate that the microbe left Africa about 55,000 years ago, just when humans did. One lineage of the microbe appears both in East Asian and in native South American populations, supporting the notion that South Americans originally came from Asia.

### ALL ABOUT EVE

THE FAST, relatively predictable rate of "neutral" mitochondrial mutations—ones that are neither beneficial nor harmful—lets the organelles operate as molecular clocks. Counting the differences in the number of mutations (ticks of the clock) between two groups, or lineages, allows a researcher to construct a genetic tree that tracks back to a common ancestor—Mitochondrial Eve or another woman who founded a new lineage. Comparison of the ages of the lineages from different regions permits the building of a timeline of human migrations.

Since 1987 the data bank on human diversity has broadened to encompass the Y chromosome—the sex chromosome passed down only by males to their sons. The male-transmitted DNA carries many more nucleotides than mitochondrial DNA does (tens of millions, as opposed to just 16,000), enhancing investigators' ability to distinguish one population from another. Analyzing mitochondrial and Y chromosome DNA from human populations has turned up hundreds of genetic markers (DNA sites

PETER HAWTIN *University of Southampton/Photo Researchers, Inc*



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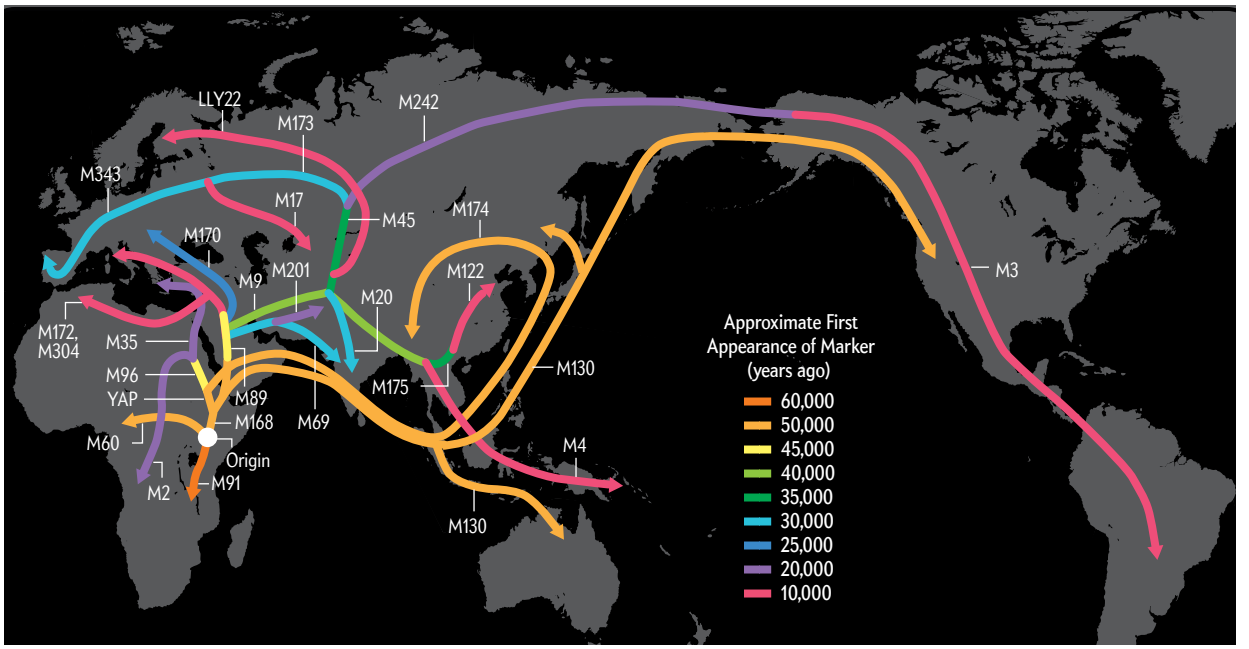
# Tracking Y Chromosomes through Time

**Geneticists can track the path** of ancient migrations by examining genetic markers in Y chromosomes from men who hail from different parts of the world. Each marker, such as M168 or M89, identifies a lineage of men and where the lineage originated. By building an evolutionary tree based on observing many living people with the markers, investigators can determine the approximate ages of the lineages.



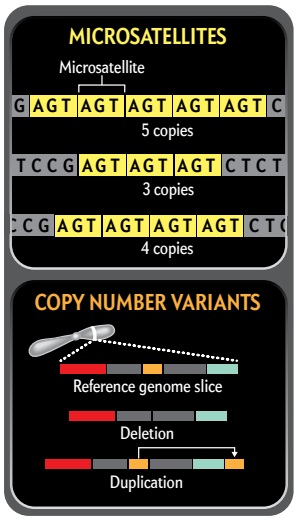

having identifiable mutations specific to particular lineages).

The route humans took from Africa to the Americas over the course of tens of thousands of years can now be tracked on the map as if the travelers were moving, albeit extremely slowly, on a series of interconnected superhighways. Alphanumeric route signs, such as I-95, can be recast as alphanumeric genetic markers. In the case of the Y chromosome, for instance, cross the Bab el Mandeb on highway (genetic marker) M168, which becomes M89 when heading north through the Arabian Peninsula. Make a right at M9 and set out toward Mesopotamia and beyond. Once reaching an area north of the Hindu Kush, turn left onto M45. In Siberia, go right and follow M242 until it eventually traverses the land bridge to Alaska. Pick up M3 and proceed to South America [*see map above*].

Mitochondrial DNA and the Y chromosome remain powerful analytical instruments. The National Geographic Society, IBM and the Waitt Family Foundation joined in privately funded research that is primarily devoted to using these tools. With the help of 10 regional academic institutions, the so-called Genographic Project has so far gathered DNA from more than 500,000 people worldwide, including around 75,000 indigenous people. "What we're focusing on are the details of how people made the journeys," says Spencer Wells, who heads the project. In one report its researchers found that the Khoisan people of southern Africa remained genetically separate from other Africans for 100,000 years. In another study, they demonstrated that some of the gene pool of Lebanese men can be traced to Christian Crusaders and Muslims from the Arabian Peninsula.

## POWER TOOLS

GENETIC RESEARCHERS have sampled the DNA of many people living along the migratory routes they have discovered. Yet the seeming certainty of the data sometimes deceives. Scientists who study human origins still would prefer a fossil they can hold in their hands over a genealogical tree. DNA differs from the radioactive isotopes used to date fossils. The rate of mutation can fluc-




JEN CHRISTIANSEN; SOURCE: NATIONAL GEOGRAPHIC MAPS

## MANY WAYS TO SLICE A GENOME

**Scientists continually seek** genetic markers—characteristic patterns of nucleotides—that differ from one population group to another and that can be used when comparing whole genomes. Microsatellites, short repetitive nucleotide segments found on all the chromosomes (*top*), have served as markers for a number of years. A new type of whole-genome analysis looks for what are called copy number variants—deletions or duplications of up to one million nucleotides (*bottom*).



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tuate from one stretch of DNA to another.

But paleoanthropologists are in a fix. Fossil remains are rare and too often incomplete. The earliest migration from Africa to Australia shows up in mitochondrial and Y genetic material (thanks to Andaman Islanders, among others), yet the physical artifacts are largely missing along the route.

The answer to the absence of stones and bones: more DNA, from wherever. To bolster the case for genetics, researchers have looked to microbes that have hitched a ride on humans, inspecting their genes to look for similar patterns of migration. Freeloaders include bacteria, viruses and even lice. Besides microorganisms, the Human Genome Project and related efforts to look across the expanse of whole genomes have yielded a set of power tools that are helping to compensate for deficiencies in genetic methods. "You can look at so many different places in the genome from many individuals and in many populations to achieve more statistical power in testing different hypotheses," says Tim Weaver, a professor of anthropology at the University of California, Davis.

## JUST LOOK IN THE PHONE BOOK

**The genetic record** of human history may be bolstered by simply paging through a phone book for certain names. A team led by Mark A. Jobling of the University of Leicester reported in 2007 that men in northwestern England with surnames that had been used there before 1600 had high levels of Scandinavian ancestry on their Y chromosomes, a legacy of a Viking heritage. Jobling has suggested in another paper that criminal investigators might be able to use this method to link DNA evidence to a set of surnames to narrow down a pool of suspects.

For more than a decade researchers have made dramatic discoveries by simultaneously comparing a multitude of variable, or polymorphic, sites interspersed throughout the genome's three billion nucleotides. The first whole-genome studies earlier in the 2000s looked at differences among populations in short repetitive stretches of DNA known as microsatellites. Since then, the scope afforded by whole-genome scans has widened further. In February 2008 two papers, one in *Science,* the other in *Nature,* reported the largest surveys to date of human diversity. Both examined more than 500,000 single nucleotide polymorphisms (SNPs)—swaps of one nucleotide for another at a particular spot in the DNA—from the Human Genome Diversity Panel. These cell lines were drawn from more than 1,000 individuals from 52 populations worldwide and are maintained by the Center for the Study of Human Polymorphisms in Paris.

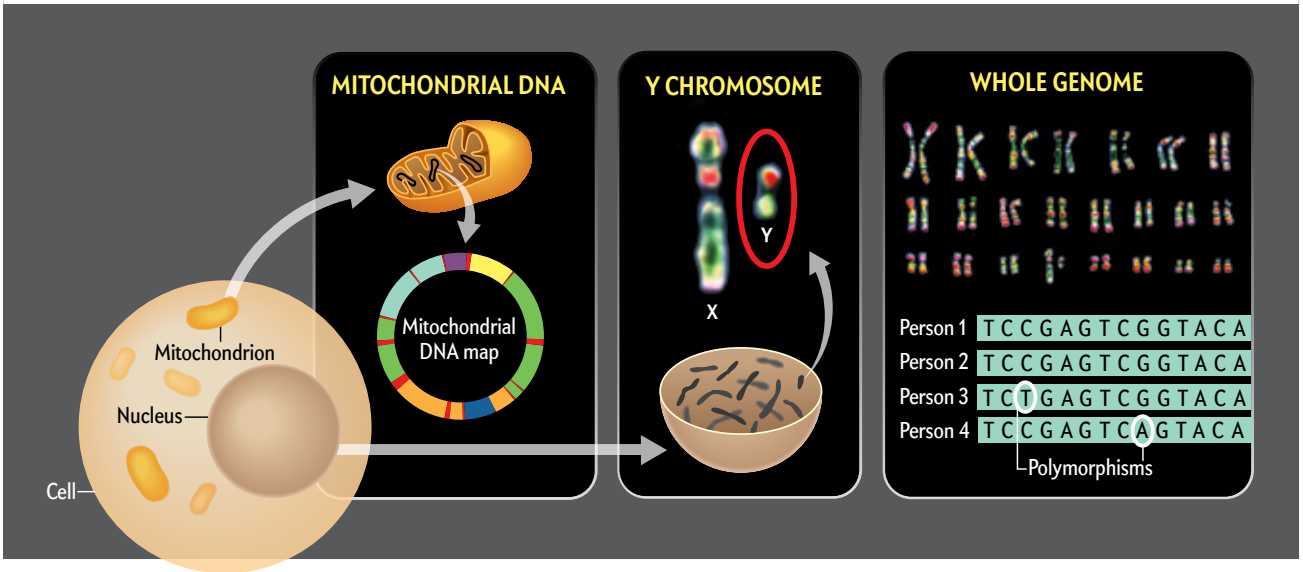
The two research teams analyzed the wealth of data in various ways. They compared SNPs directly among distinct populations. They also looked at haplotypes, blocks of DNA containing numerous SNPs that are inherited intact through many generations. The group that wrote the *Nature* paper also explored a new technique for surveying human variation by comparing repetitions or deletions of DNA stretches of up to a million nucleotides long (copy number variations) throughout a person's genome, consistent with the larger trend to mine the genome for ever more markers of variation. "Any one piece of the genome will have a history that doesn't necessarily reflect the ancestry of the genome as a whole," says Noah A. Rosenberg, now at Stanford University and one of the authors of the *Nature* paper. But looking at many areas at once, he explains, can overcome that problem: "With thousands of markers, it's possible to determine the overall story of human migrations."

Looking at hundreds of thousands of SNPs allowed the researchers to resolve the identities of individual populations—and to see

METHODS

## Genetic Prospecting

**Digging through DNA** to find the origins of the first modern humans began 20 years ago through inspection of genetic material in the cell's mitochondria and later in the Y chromosome. Today investigations can scan sections of the whole genome contained in the cell nucleus to compare differences, or polymorphisms, in large numbers of individual nucleotides, the "letters" of the DNA alphabet.




JEN CHRISTIANSEN; CNRI/PHOTO RESEARCHERS, INC. (*chromosome images*)



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how genetically close relations spread far and wide. Native South American ancestry was tracked back to Siberians and some other Asians. The Han people, China's principal ethnic group, has distinct northern and southern populations. Bedouins are related to groups from Europe and Pakistan as well as the Middle East.

The findings, which jibed with previous research from anthropology, archaeology, linguistics and biology (including previous mitochondrial and Y DNA studies), also provided a broader statistical foundation for the out of Africa hypothesis, supporting the idea that a small population of humans moved out of the continent, then grew in size in a new home until another subgroup of "founders" broke off and moved away—a process that repeated itself until the entire world was settled. These wayfarers edged out archaic human populations—*Homo neanderthalensis* and *Homo erectus*. The new DNA work indicates that each time a smaller group split off, it carried only a subset of the genetic diversity originally present in the African population. So as distance (and time) removed from Africa lengthens, diversity diminishes, providing a means to follow population movements. Native Americans, sojourners on the last major continental migrations, have much less variety in their genomes than Africans do.

Many scientists believe that the weight of evidence, now backed by large statistical analyses such as the ones in *Science* and *Nature,* gives the out of Africa proponents a clear edge in a long-running debate over human origins. The multiregional hypothesis—a competitor to the out of Africa one—argues that populations that descended from archaics, such as *H. erectus,* evolved over the past 1.8 million years in Africa, Europe and Asia and gradually emerged as *Homo sapiens*. Occasional interbreeding ensured that the groups did not split off into separate species.

Few scientists still hold a banner for a strict interpretation of multiregionalism. But modified versions still circulate, mostly as attempts to pinpoint whether *H. sapiens* bear genetic signatures of our encounters with hominid cousins. Vinayak Eswaran of the Indian Institute of Technology, aided by Henry C. Harpending and Alan R. Rogers of the University of Utah, has come up with a set of simulations that suggest that after humans migrated out of Africa they interbred extensively with archaic species such as *H. erectus*. Eswaran's model suggests that as much as 80 percent of the modern human genome may have been subject to the effects of this kind of interbreeding.

The genetic imprint is not as visible as might be expected if interbreeding occurred, but Harpending offers an explanation. A set of beneficial genes carried by African emigrants, perhaps ones that assisted in childbearing, brought a selective advantage that eventually blotted out the signature of some archaic genes. "The result is that the population seems more closely related to the [African] source population of the favored genes than it really is," he says.

**CONTAMINATION** from human DNA complicates genetic analyses of Neandertals. Workers in El Sidron Cave in Spain wore clean-room suits to protect newly excavated samples.

COURTESY OF CONSEJO SUPERIOR DE INVESTIGACIONES CIENTÍFICAS

### ARE WE PART NEANDERTAL?

THOSE SIMULATIONS are no longer figments of a computer model. Some fossilized skeletal remains of *H. sapiens* have features that are reminiscent of earlier hominids, and the genetic record of contemporary humans has also provided increasing fuel for discussion.

Continued advances in gene-sequencing techniques have meant that the Max Planck Institute for Evolutionary Anthropology in Leipzig has succeeded in sequencing the genomes of Neandertals and another recently discovered extinct hominid, the Denisovans. It turns out that *H. sapiens*, except in Africa, did engage in interhominid trysts. Representatives of our species outside of that continent have 2.5 percent Neandertal DNA, and some of those in Oceania bear a 5 percent genetic imprint from Denisovans as well as a complement of Neandertal DNA. Moreover, 1 percent of the DNA of Southeast Asians comes from Denisovans.

The actual sequencing effort turned into a gargantuan project. Handling or even breathing on a sample can be an impediment to working with ancient DNA: some anthropologists wrap themselves in the clean-room "bunny suits" used in microchip factories when they head to the field on a dig. In the laboratory at Max Planck, researchers place tags made up of four nucleotides of synthetic DNA at the beginning of each strand of Neandertal genetic material. Once



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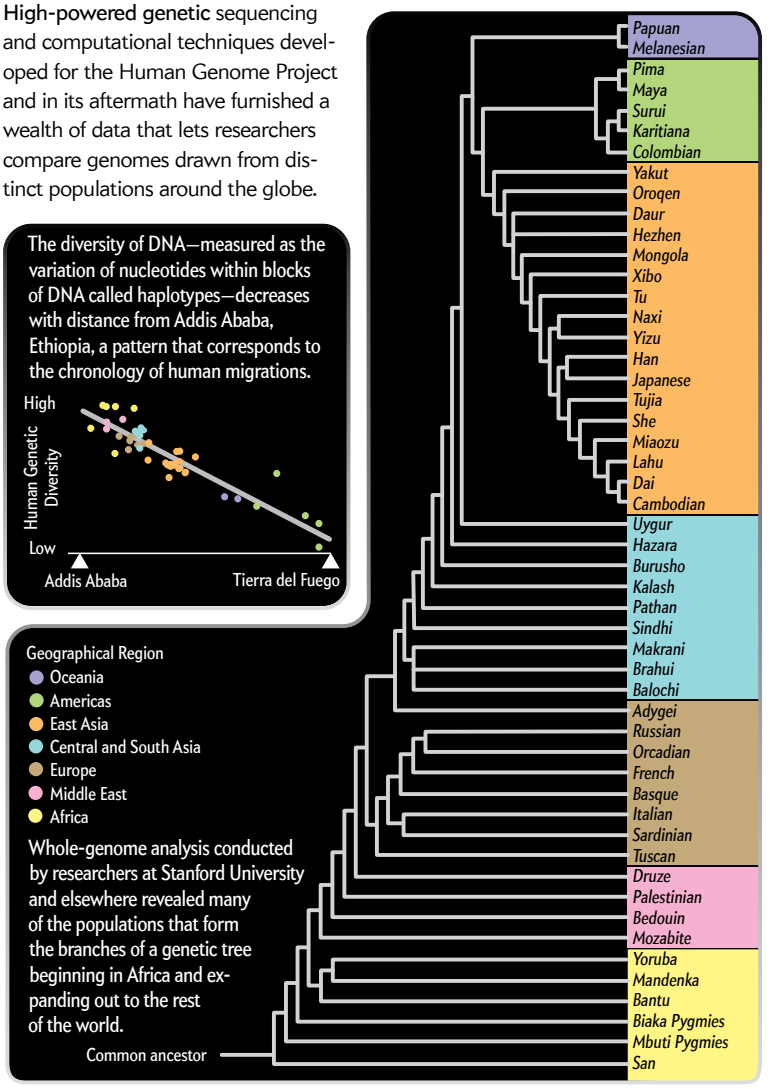
# Far and Wide

**High-powered genetic** sequencing and computational techniques developed for the Human Genome Project and in its aftermath have furnished a wealth of data that lets researchers compare genomes drawn from distinct populations around the globe.




**A genomic map of the world,** crafted by researchers at the University of Michigan, shows that genetic diversity decreases outside of Africa. Each colored tile represents a common haplotype. Africa has more tiles than found on other continents and ones that correspond to haplotypes found nowhere else.

each strand exits the sequencing machine, it goes through a molecular identity check.

### HOW HAVE WE ADAPTED?

AS RESEARCHERS continue sequencing DNA from shards of old bone to explore whether humans mated with other species of the genus *Homo,* other investigators are applying genome-wide analyses of DNA to see which genetically controlled traits changed through genetic drift (random mutations) and natural selection as migrants adapted to their new homes.

A second study in February 2008 in *Nature* showed the consequences of the declining genetic diversity as humans left Africa. The project compared 40,000 SNPs from a group of 20 European-Americans and 15 African-Americans. It found that the European-Americans had a higher proportion of harmful genetic changes, ones potentially related to disease, than the African-Americans did, although the authors refrained from speculation about any specific health effects. The research shows what lead scientist Carlos D. Bustamante called a "population genetic echo" of Europe's founding. The low genetic diversity of Europe's small initial population allowed a set of harmful mutations to disperse widely and new harmful ones to emerge when the numbers of people began to grow. Natural selection has not yet had time to remove deleterious changes.

Genome-wide research is also starting to furnish a panoramic picture of how natural selection helped migrants adapt to new environs. A spate of recent studies have looked for genetic alterations that have occurred since humans left Africa or took up agriculture and that appear to have been useful for surviving in novel circumstances. Genetic prospectors mined the International HapMap, a catalogue of haplotypes and the 3.9 million SNPs contained therein from North Americans with ancestry in northwestern Europe and from individuals sampled in Nigeria, China and Japan.

One study, co-authored by Harpending, showed that the rate of change of DNA, and thus the pace of evolution, has accelerated over the past 40,000 years. Another by Pardis C. Sabeti of the Broad Institute in Cambridge, Mass., and her colleagues indicated that hundreds of regions of the genome are still undergoing selection, including areas that govern resistance to disease, development of skin color, and hair follicles, which regulate sweat. Such findings imply that human populations are continuing to adapt to

JEN CHRISTIANSEN (*graph and genetic tree*); COURTESY OF MARTIN SOAVE *University of Michigan (map)*; SOURCE: "WORLDWIDE HUMAN RELATIONSHIPS INFERRED FROM GENOME-WIDE PATTERNS OF VARIATION," BY JUN Z. LI ET AL., IN *SCIENCE*, VOL. 319; 2008



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# Can You Spare Some DNA?

In their quest for a more in-depth picture of human origins, geneticists need more samples from indigenous populations the world over. "There's a need for greater resolution in the data," says Marcus W. Feldman of Stanford University and a co-author of a whole-genome comparative analysis. "If you were to give me $1 million tomorrow, I'd find 100 more populations out of the 5,000 we need."

An equal hurdle may be overcoming objections to this kind of research. In 1991 Luigi Luca Cavalli-Sforza and his colleagues outlined a vision for the Human Genome Diversity Project, which would have created a store of cells from 25 unrelated individuals from each of some 400 populations worldwide. The project foundered, however, because of resistance from indigenous groups to providing samples: one group called it a "Vampire Project." Despite extensive informed consent procedures, some groups worried about whether the samples would be used in research for patenting and developing new drugs, which they considered to be a form of biopiracy.

The project never received more than planning support from the federal government, but a more modest version began more than a decade ago, based on cell lines that various population geneticists had brought together on their own from more than 1,000 individuals. This collection, known as the Human Genome Diversity Panel, is stored at the Center for the Study of Human Polymorphisms in Paris. So far it has provided a database containing information on 52 populations that has been used for various studies, including two large, transgenomic investigations reported in *Nature* and *Science* in February 2008.

**COLLECTION OF DNA** for the Genographic Project moves forward in Chad. Spencer Wells, who heads the project, takes a cheek swab.

Like the Human Genome Diversity Project, the more recent Genographic Project, which has gathered DNA from about 75,000 indigenous people so far, also faced opposition. The project has careful protocols for ensuring informed consent in sample gathering, and it has not made collections for medical research. Yet it has still run into resistance, in particular, from Native American groups.

No matter what assurances are given, some groups will be reluctant to yield a cheek swab or blood sample. Investigators in this field may never achieve their goal of obtaining a set of samples that fully reflects every subtle gradation of human genetic diversity. —*G.S.*

DAVID EVANS *National Geographic*

regional differences in sun exposure, foods and pathogens they encountered when they left their ancestral African home. And Africans have evolved as their environs changed.

One study led by Lluis Quintana-Murci of the Pasteur Institute in Paris showed that 580 genes, including ones that play a role in diabetes, obesity and hypertension, are undergoing selection differently among the HapMap populations, perhaps explaining geographical differences in disease patterns and providing clues to new targets for developing drugs.

Consideration of the processes underlying human diversity of course moves beyond the dimensions of hair follicles and the ability to digest milk. Scientific debate over what constitutes race and ethnicity can quickly enter the picture. What does it mean if a gene variant related to cognition is found more in Europeans than in Africans? Better public understanding of genetics—that a single gene does not act like a light switch that toggles between intelligence and doltishness—may quell misguided speculations.

Genetic literacy will let a term like "Asian" or "Chinese" be replaced by more subtle classifications based on the differences in ancestral genetic makeup found in recent genome-wide scans, such as the distinction between China's Han groups. "There is no race," Quintana-Murci says. "What we see [from the standpoint of genetics] is geographical gradients. There are no sharp differences between Europeans and Asians. From Ireland to Japan, there is no sharp boundary where something has changed completely."

The journey through evolutionary history set in place by comparative genomics is still starting. In the meantime, the hunger for more data and more powerful computers and algorithms knows no limits. Amassing larger databases—an international consortium announced in January 2008 is proceeding with the sequencing of 1,000 genomes from various regional populations—will let researchers run ever more realistic simulations of alternative models of human evolution and weigh the probabilities of each one, yielding the best picture yet of who we are and where we came from. SA

**GARY STIX** is a senior editor at *Scientific American*.

MORE TO EXPLORE

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ARCHAEOLOGY

# The First Americans

**Humans colonized the New World earlier than previously thought—a revelation that is forcing scientists to rethink long-standing ideas about these trailblazers**

BY HEATHER PRINGLE

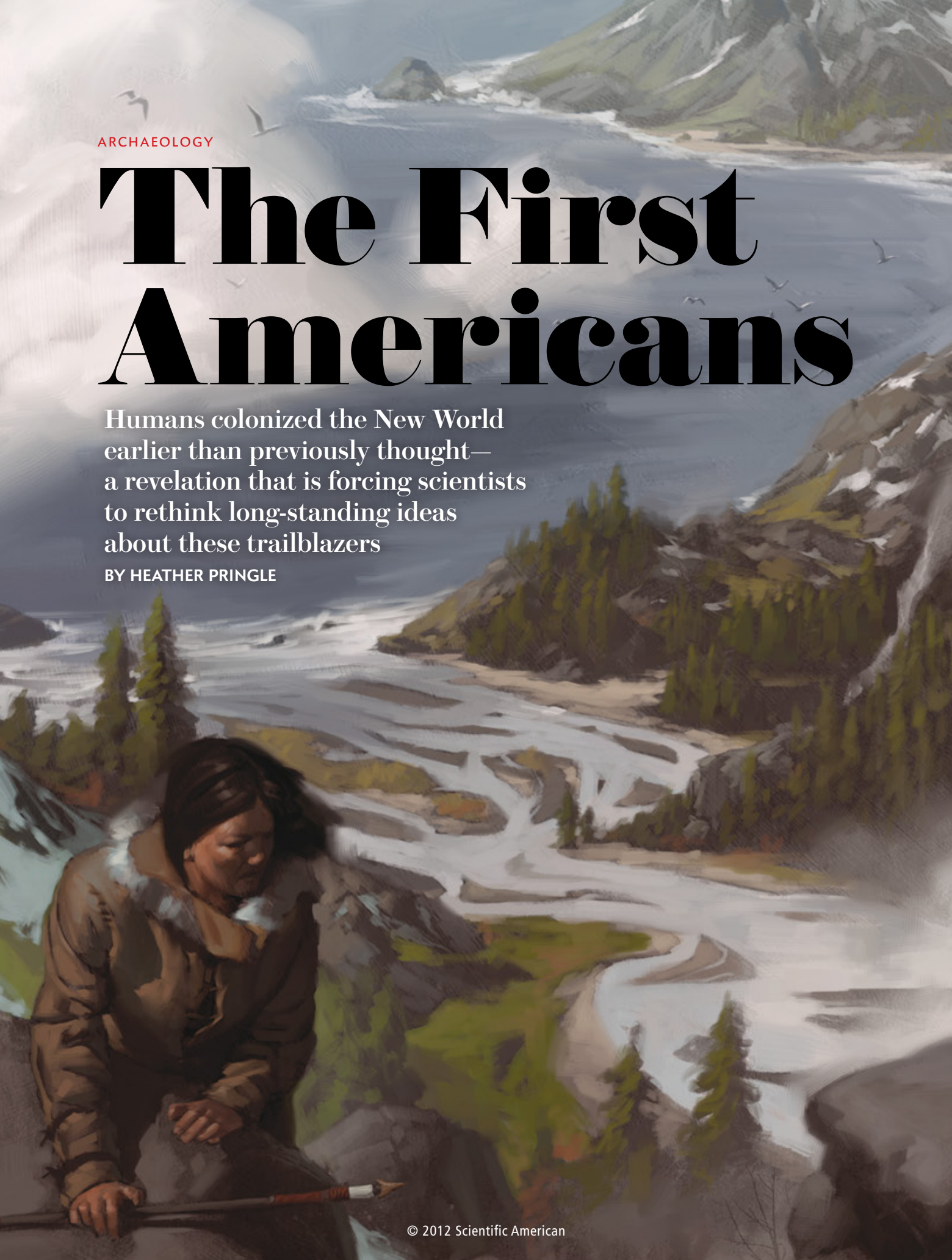

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*Illustration by Tyler Jacobsen*



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IN THE SWELTERING HEAT OF AN EARLY JULY AFTERNOON, Michael R. Waters clambers down into a shadowy pit where a small hive of excavators edge their trowels into an ancient floodplain. A murmur rises from the crew, and one of the diggers gives Waters, an archaeologist at the Center for the Study of the First Americans at Texas A&M University, a dirt-smeared fragment of blue-gray stone called chert. Waters turns it over in his hand, then scrutinizes it under a magnifying loupe. The find, scarcely larger than a thumbnail, is part of an all-purpose cutting tool, an ice age equivalent of a box cutter. Tossed away long ago on this grassy Texas creek bank, it is one among thousands of artifacts here that are pushing back the history of humans in the New World and shining rare light on the earliest Americans.

Waters, a tall, rumpled man in his mid-fifties with intense blue eyes and a slow, cautious way of talking, does not look or sound like a maverick. But his work is helping to topple an enduring model for the peopling of the New World. For decades scientists thought the first Americans were Asian big-game hunters who tracked mammoths and other large prey eastward across a now submerged landmass known as Beringia that joined northern Asia to Alaska. Arriving in the Americas some 13,000 years ago, these colonists were said to have journeyed rapidly overland along an ice-free corridor that stretched from the Yukon to southern Alberta, leaving behind their distinctive stone tools across what is now the contiguous U.S. Archaeologists called these hunters the Clovis people, after a site near Clovis, N.M., where many of their tools came to light.

Over the past decade or so this Clovis First model has come under sharp attack as a result of new discoveries. In southern Chile, at a site known as Monte Verde, archaeologist Thomas D. Dillehay, now at Vanderbilt University, and his colleagues found traces of early Americans who slept in hide-covered tents and dined on seafood and a wild variety of potato 14,600 years ago, long before the appearance of Clovis hunters. Intrigued by the findings, some scientists began looking for similar evidence in North America. They found it: in Paisley Five Mile Point Caves in Oregon, for example, a team uncovered 14,400-year-old human feces flecked with seeds from desert parsley and other plants—not the kinds of comestibles that advocates of the big-game hunters scenario expected to find on the menu.

Now, along Buttermilk Creek, Waters and his team have made one of the most important finds yet: a mother lode of stone tools dating back a stunning 15,500 years ago. In all, the team has excavated more than 19,000 pre-Clovis artifacts—from small blades bearing tiny wear marks from cutting bone to a polished chunk of hematite, an iron mineral commonly used in the Paleolithic world for making a red pigment. Publicly unveiled in the spring of 2011, the site has yielded more pre-Clovis tools than all other such sites combined, and Waters has spared no expense in dating each layer multiple times. "It is easily the best evidence for pre-Clovis in North America," says Vance T. Holliday, an anthropologist and geoscientist at the University of Arizona.

Energized by such finds, archaeologists are now testing new models for the peopling of the New World. Drawing on evidence from a range of sciences—from genetics to geology—they are searching for answers to a host of pressing questions: Where did the earliest Americans come from? When exactly did they arrive, and what route did they take into the New World? For the first time in decades there is a heady whiff of discovery in the air. "We are now addressing the big issues," says James M. Adovasio, an archaeologist at Mercyhurst College. "We are looking at the circumstances of the dispersal of humans into the last great habitat on the planet."

## GENETIC TRAILS

THE PEOPLING OF THE NEW WORLD, from the blustery cold of the Arctic to the sultry heat of the Amazon and the stormy winds of Tierra del Fuego, remains one of humanity's greatest achievements, a feat of endurance and adaptation not to be equaled, in the view of the famous 20th-century French archaeologist François Bordes, "until man lands on a planet belonging to another star." Yet archaeologists have long struggled to uncover the beginnings of this transcontinental adventure, given the daunting task of locating the early campsites of a tiny population of highly mobile hunters and gatherers in the vast northern wildernesses of North America and Asia. Over the past decade, however, geneticists have taken the search for the first Americans to the molecular level, finding new clues to where they hailed from and when they left their homeland in the DNA of indigenous peoples.

In more than a dozen studies geneticists examined modern and ancient DNA samples from Native Americans, looking for telltale genetic mutations or markers that define major human lineages known as haplogroups. They found that native peoples in the Americas stemmed from four major founding maternal haplogroups—A, B, C and D—and two major founding paternal haplogroups—C and Q. To find the probable source of these haplogroups, the teams then searched for human populations in the Old World whose genetic diversity encompassed all the lineages. Only the modern inhabitants of southern Siberia matched this

IN BRIEF

**Archaeologists long thought** the first Americans were the Clovis people, who were said to have reached the New World some 13,000 years ago from northern Asia.

**But fresh archaeological finds** prove that humans reached the Americas thousands of years before that. **These discoveries,** along with insights from genetics and geology, have prompted reconsideration of where these pioneers came from, when they arrived and what route they took into the New World.



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genetic profile, a finding that strongly indicates that the ancestors of the first Americans came from an East Asian homeland.

This evidence confirmed what most archaeologists suspected about the location of this homeland. It also strongly suggested that the timing proposed in the Clovis First scenario was wrong. Geneticists now calculate, based on mutation rates in human DNA, that the ancestors of the Native Americans parted from their kin in their East Asian homeland sometime between 25,000 and 15,000 years ago—a difficult time for a great northern migration. Huge glaciers capped the mountain valleys of northeastern Asia, at the same time massive ice sheets mantled most of Canada, New England and several northern states. Indeed, reconstructions of past climate based on data preserved in ice cores from Greenland and on measurements of past global sea levels show that these ice sheets reached their maximum extent in the last glacial period between at least 22,000 and 19,000 years ago. "But these folks were extraordinarily adept at moving over the landscape," says David Meltzer, an archaeologist at Southern Methodist University. "Their entire existence—and the existence of everyone they knew and the existence of their ancestors—was about adapting. They had a toolbox of tactics and strategies."

Dressed in warm, tailored hide garments stitched together with sinew and bone needles and armed with an expert knowledge of nature, the ancestors of the Paleo-Americans entered an Arctic world without parallel today. The ice sheets in northern Europe and North America had locked up vast quantities of water, lowering sea level by more than 100 meters and exposing the continental shelves of northeastern Asia and Alaska. These newly revealed lands, together with adjacent regions in Siberia, Alaska and northern Canada, formed a landmass that joined the Old World seamlessly to the New.

Known today as Beringia, this landmass would have made a welcoming way station for pre-Clovis migrants. The air masses that swept over it were so dry they brought little snowfall, preventing the growth of ice sheets. As a result, grasses, sedges and other cold-adapted plants thrived there, as shown by plant remains found preserved under a layer of volcanic ash in northwestern Alaska and in the frozen intestines of large herbivores that once grazed in Beringia. These plants formed an arid tundra-grassland, and there woolly mammoths weighing as much as nine tons grazed, as did giant ground sloths, steppe bison, musk ox and caribou. Genetic studies of modern Steller's sea lion populations suggest that this sea mammal likely hauled out on the rocks along Beringia's island-studded south shore. So the migrants may have had their pick not only of terrestrial mammals but also of seafaring ones.

Received wisdom holds that the trailblazers hurried across Beringia to reach warmer, more hospitable lands. Some researchers, however, think the journey could have been a more leisurely affair. The major genetic lineages of Native Americans possess many widespread founding haplotypes—combinations of closely linked DNA sequences on individual chromosomes that are often inherited together—that their closest Asian kin lack. This suggests

COURTESY OF MICHAEL R. WATERS *Texas A&M University*

**DIG NEAR** Buttermilk Creek in Texas has yielded artifacts that clearly predate the Clovis culture. Hunters may have come here to exploit the local chert stone to make tools.

the earliest Americans paused somewhere en route to the New World, evolving in isolation for thousands of years before entering the Americas. The most likely spot for this genetic incubator is Beringia. There the migrants could conceivably have been cut off from their Asian kin as the climate cooled some 22,000 years ago, forcing Siberian bands to retreat south.

Whether the migrants cooled their heels in Beringia, however, or somewhere else in northeastern Asia, people eventually began striking off farther east and south. A warming trend began slowly shrinking North America's ice sheets some 19,000 years ago, gradually creating two passable routes to the south and opening the possibility of multiple early migrations. According to several studies conducted over the past decade on the geographical distribution of genetic diversity in modern indigenous Americans, the earliest of these migrants started colonizing the New World between 18,000 and 15,000 years ago—a date that fits well with emerging archaeological evidence of pre-Clovis colonists. "At some point, these migrants surveyed the landscape and realized for the first time that smoke from all the other campfires was behind them, and ahead there was no smoke." Adovasio reflects. "And at that moment, they were literally strangers in a strange land."

## A COASTAL ROUTE

ARCHAEOLOGISTS take up the tale of the earliest Americans as these travelers pushed southward, exploring a wilderness untouched by humans. In an office decorated with prints and pictures of sharks and a poster of a traditional Chumash wood canoe, Jon M. Erlandson, an archaeologist at the University of Oregon, mulls over new evidence of their journey. Reed-thin, tousled and in his mid-fifties, Erlandson has spent much of his career digging at sites along the coast of California, becoming one of the foremost proponents of what is often called the coastal route theory. Whereas supporters of the Clovis First model envisioned humans

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# A Precocious Peopling

**In the traditional view** of human colonization of the Americas, big-game hunters from Asia—the so-called Clovis people—swept quickly across a now submerged landmass called Beringia into North America around 13,000 years ago and hastened south into warmer climes. Over the past decade, however, evidence against this Clovis First scenario has mounted. The latest geologic and archaeological research indicates that humans entered the New World thousands of years before the Clovis people left behind their distinctive stone tools and suggests two possible migration paths: a coastal route and an early ice-free corridor.

## Land Route: Ice-Free Corridor

According to the Clovis First model, the Cordilleran and Laurentide ice sheets did not part ways until 13,000 years ago, thus barring a pre-Clovis overland migration into the Americas. But fresh geologic data indicate that the corridor opened by 15,000 years ago. Travelers along this route may have hunted birds and brought dogs with them to carry their gear. Trekking 16 kilometers a day, the migrants could have reached the end of the corridor in four months.

Actual size

**KEY FIND: SANTA ROSA ISLAND, CALIF.**

Distinctive, Christmas tree–shaped stone points found at Santa Rosa Island date to 11,800 years ago and resemble stone tools from East Asia that date to 15,000 years ago, hinting at an early migration route along the northern Pacific Rim.

**FAMOUS ASSEMBLAGE: CLOVIS, N.M.**

In the 1930s discoveries at Blackwater Locality No. 1 near Clovis, N.M., and other sites yielded long, sturdy, fluted spearpoints for hunting large-game animals such as woolly mammoths. For years these Clovis points and other artifacts had the distinction of being the oldest in the New World and formed the basis of the Clovis First model of the peopling of the Americas.



Actual size

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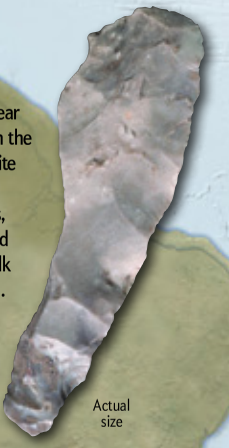
## Coastal Route

Explorers from East Asia may have paddled small boats to southern Beringia and down the western coast of the Americas starting as early as 16,000 years ago. The British Columbian coast was rid of ice by then, and migrants would have had access to a bounty of marine mammals and fish. The earliest known site near the coast, Monte Verde in Chile, dates to just 14,600 years ago; however, the thawing of the ice sheets during the last glacial period may have drowned the oldest sites along the ancient coastline.

PACIFIC OCEAN

**KEY FIND: FRIEDKIN SITE, TEX.**

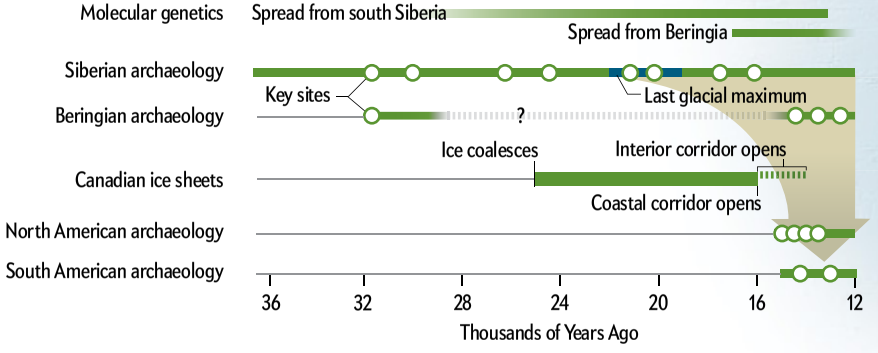
With thousands of artifacts securely dated to 15,500 years ago, this site near Buttermilk Creek in Texas is the nail in the coffin of the Clovis First theory. Despite their antiquity, the remains exhibit features in common with Clovis tools, hinting that Clovis hunters descended from bands like the ones at Buttermilk Creek, rather than originating in Asia.



Actual size

SOUTH AMERICA

Monte Verde, Chile




## Lines of Evidence

Taken together, genetic, archaeological and geologic records suggest that humans set out from Siberia sometime between roughly 25,000 and 15,000 years ago, entering the New World via Beringia as the ice sheets blanketing the Pacific coastal corridor and the interior corridor of North America receded. By 14,600 years ago they had made their way to South America.

*Illustration by Tyler Jacobson, Map by XNR Productions*

COURTESY OF JON M. ERLANDSON *University of Oregon (Santa Rosa spearhead)*; COURTESY OF MICHAEL R. WATERS *Texas A&M University (Clovis and Friedkin spearheads)*; FROM "THE LATE PLEISTOCENE DISPERSAL OF MODERN HUMANS IN THE AMERICAS," BY TED GOEBEL ET AL., IN *SCIENCE*, VOL. 319; MARCH 14, 2008 *(timeline: glacial maximum and corridor opening dates have been updated with other sources)*; CONSULTANTS: KENNEDY MUNYIKWA *Athabasca University* AND MICHAEL R. WATERS *(ice sheets)*; QUENTIN MACKIE *University of Victoria (coastal route vignette)*; STUART J. FIEDEL *Louis Berger Group* AND BEN POTTER *University of Alaska Fairbanks (land route)*

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reaching the Americas by trekking overland, Erlandson thinks the earliest travelers arrived by sea, paddling small boats from East Asia to southern Beringia and down the western coast of the Americas. Now he and his colleague Todd J. Braje of San Diego State University have uncovered key new evidence of ancient mariners who set out in East Asia and ended their journey in Chile.

Scientists first began thinking about this coastal route in the late 1970s, when archaeologist Knut Fladmark, now a professor emeritus at Simon Fraser University in British Columbia, started examining geologic and pollen records to reconstruct ancient environments along Canada's western coast. At the time, most experts believed that the entire northwestern coast lay under thick ice until the end of the last glacial period. Analyses published in the 1960s and 1970s of ancient pollen from coastal bogs, however, showed that a coniferous forest thrived on Washington's Olympic Peninsula 13,000 years ago and that other green refugia dotted the coast. Early humans camping in these spots, Fladmark concluded, could have fueled up on seafood, from shellfish to migrating pink salmon. They may also have hunted waterfowl migrating along the Pacific flyway, as well as caribou and other hardy land animals grazing in the larger refugia.

Archaeologists now know that much of the British Columbian coast was free of ice at least 16,000 years ago. Although they have yet to find any preserved boats in early American coastal sites, many researchers think such watercraft were probably available to these wayfarers: at least 45,000 years ago humans voyaged and island-hopped all the way from Asia to Australia. Traveling by water down the western coast of the New World would have been easier in many respects than trekking overland. "It's an environment that's relatively similar along a north-south transect, which makes it a path of least resistance," says Quentin Mackie, an archaeologist at the University of Victoria in British Columbia.

Still, finding campsites of early mariners has proved a tall order for scientists. As the ice sheets of the last glacial period thawed, the meltwater raised sea level, drowning ancient coastlines under meters of water. In March 2011, however, Erlandson and Braje detailed in the journal *Science* striking evidence of early seafarers at a newly discovered site on Santa Rosa Island located just off the southern California coast. Nearly 12,000 years ago Paleo-American sailors crossed 10 kilometers of open water to reach Santa Rosa, a journey that would have required a boat.

The island site lies near the mouth of an inland canyon and close to what might have been an ancient marsh. Erlandson and his team found human refuse buried in the sediments, including bird bones and charcoal the researchers radiocarbon-dated to 11,800 years ago. Early coastal hunters had dined there on birds such as Canada geese and cormorants, as well as on pinnipeds, a group that encompasses seals and sea lions. The hunters also left behind traces of a distinctive technology: more than 50 dainty stemmed points that looked in outline like little brown Christmas trees. Such points may have tipped darts for hunting birds or small marine mammals. "They are just extremely thin and extremely well made," Erlandson says. Overall, their design and manufacture seemed very unlike the long, furrowed and sturdy-looking Clovis spearpoints used by big-game hunters on the mainland.

Curious about the origin of this coastal technology, Erlandson and Braje scoured published archaeological reports on other sites for clues. They discovered that excavators had dug up very similar stemmed points at ancient sites scattered around the northern rim of the Pacific Ocean. The earliest came from East Asia—the Korean peninsula, Japan and the Russian Far East—and all dated to around 15,000 years ago. Moreover, the farther one traveled away from there, the younger these weapons were, with 14,000-year-old stemmed points in Oregon and 12,000-year-old points on the Channel Islands, in Baja California and along coastal South America. Erlandson shakes his head in wonderment. "Some of the point assemblages in Japan are really similar to the ones in the Channel Islands," he says.

**It was a land empty of human rivals, a new world of possibilities.**

Erlandson and Braje now think this trail of technology marks out an early migration route along the northern Pacific Rim, a coastal highway loaded with food. Kelp, for example, flourishes in the cold, nutrient-rich waters there, forming coastal marine forests that harbor species ranging from rockfish to abalone to sea otters. Such marine forests would likely have thrived along Beringia's southern coast even during the last glacial period. Studies of ocean temperature some 18,000 years ago suggest that sea ice formed only in winter along Beringia's southern coast, and this seasonal deep freeze would not have eradicated the great marine forests. "And it's not just kelp that would have facilitated a coastal migration," Erlandson says. "There's an enormous amount of other resources in marine estuaries and in salmon streams."

Even so, Paleo-Americans exploring this rich coastal world were unlikely to have raced southward. They may have moved just a kilometer or so a year, gradually expanding the southern boundaries of their hunting and gathering territory. "This wasn't a sprint down the coast," Erlandson concludes. "You had to have marriage partners because you were moving into unpopulated lands. So you had to maintain connections with people behind you."

### AN INLAND CORRIDOR

THE WESTERN COAST of the Americas was not the only available route for early colonists. Over the past six years a team of earth scientists and dating experts led by Kennedy Munyikwa, a geologist at Athabasca University in Alberta, has been reexamining another potential passageway, one that was widely championed by supporters of the Clovis First theory but that later fell out of favor after the discovery of pre-Clovis people at the site of Monte Verde near the Chilean coast. Known as the ice-free corridor, this midcontinental route formed after North America's largest ice sheet, the Laurentide, began retreating eastward, separating from the Cordilleran ice sheet that blanketed the west, and after vast glacial lakes blocking the passageway drained, leaving dry land. The resulting corridor ran along the eastern flanks of the Rockies and extended nearly 1,900 kilometers, from Alaska to the lower 48 states.

The renewed interest in this route stems from new dates that Munyikwa and his colleagues published in June 2011 in the journal *Quaternary Geochronology*. In the 1980s researchers at the Geological Survey of Canada dated the corridor's opening by radiocarbon-testing plant remains preserved in sediments along the route. Their findings indicated that the two colossal ice sheets parted company and that the glacial lakes drained around 13,000 years ago. This time frame fit well with the Clovis First scenario,



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although it ruled out the corridor as a route for earlier people.

Yet as Munyikwa examined these early studies for a project on ancient environment change, he saw serious problems. The radiocarbon dates were few in number, and some were clearly unreliable. Moreover, the dating of plants determined when vegetation had finally reestablished itself in the corridor, not when the ice had actually retreated and the lakes drained. So Munyikwa and his colleagues decided to redate the opening of the ice-free corridor by a technique known as optically stimulated luminescence (OSL). The team focused on a section of the corridor in northern Alberta, where large sand dunes—some exceeding 10 meters in height—had formed from windblown sediments after the Laurentide ice sheet retreated.

To obtain samples for dating, Munyikwa and his team cut pits into the tallest dunes in these fields. Then they hammered black plastic pipes horizontally into the walls of these pits. Capped on one end, the pipes filled with sand that had not been exposed to sunlight since the dunes accumulated. Next the team dated each sample by the OSL method, measuring the amount of energy from environmental radiation trapped in minerals such as feldspar in the samples. The results showed that the sand dunes formed between 14,000 and 15,000 years ago, a range that likely constitutes a minimum age for the opening of the corridor, Munyikwa says, because "it's possible that the dunes formed 1,000 years after the ice went away." Moreover, the corridor in northern Alberta stretched at least 400 kilometers across at this time and likely cradled few if any large meltwater lakes. The sand that accumulated in dunes, Munyikwa points out, came from dry lake bottoms.

The big question now is whether the entire corridor lay open during this period, particularly the section to the north. Munyikwa thinks it did. His team recently dated sand dunes farther north, along the Alberta-Northwest Territory border, with similar results. The general consensus among geologists, he notes, "is that the [Laurentide] ice sheet retreated in a northeasterly direction as a wide front, as opposed to [moving] in discrete lobes. We envisage that the deglaciated land extended to the north." If so, explorers from Asia could have entered the corridor around 15,000 years ago, nearly 1,000 years after the route to the western coast opened.

The new OSL dates, says archaeologist Jack Ives of the University of Alberta in Edmonton, will prompt a fresh look at this corridor. "It is often alleged, in grave error, that the corridor region has been well investigated, when in fact it is vast, and we know little about it," Ives asserts. The oldest, broadly accepted evidence of humans in the northern corridor dates to some 12,000 years ago, but Ives thinks future archaeological surveying could well turn up much earlier sites. "I think if the coast was Highway 1, then the corridor was Highway 2," he quips.

Scoured by retreating ice and pierced by cold winds, the newly opened corridor would have seemed a formidable place to early travelers. Yet it is possible, argues Stuart J. Fiedel, an archaeologist at the Louis Berger Group, headquartered in Morristown, N.J., that hunter-gatherers in Beringia decided to explore it after watching flocks of waterfowl head south in the fall and return in the spring. Food would have been scarce, Fiedel says, but the explorers may have hunted calorie-rich birds or larger game. Recent genetic data suggest that mountain sheep grazed in two refugia in the Yukon and northern British Columbia.

As an insurance policy, the travelers may have taken along man's best friend. Hunters in Siberia seem to have first domesticated wolves as early as 33,000 years ago, based on paleontological evidence. Fiedel thinks early dogs would have made invaluable hunting companions and pack animals. In historic times, he notes, hunter-gatherers on the Great Plains used dogs to carry a variety of loads, from hides for bedding and shelter to food stores. Experiments have shown that dogs can haul about 27 kilograms, Fiedel says. Moreover, a study published in 1994 revealed that dogs carrying 13 kilograms of gear could travel as far as 27 kilometers a day, provided the temperature remained cool. If starvation threatened, the migrants could have eaten some of their dogs.

Fiedel has calculated that the colonists could have reached the southern end of the corridor in four months, traveling at a modest pace of 16 kilometers a day. As they left its stony bleakness behind, they would have laid eyes for the first time on a breathtaking abundance: warm, grassy plains filled with herds of mammoths, bison and horses; marshes and lakes dotted with waterfowl; oceans brimming with fish and marine mammals. It was a land empty of human rivals, a new world of possibilities.

## CLOVIS ORIGINS

IN THE AIR-CONDITIONED HOUSE that serves as the field-camp headquarters at Buttermilk Creek, Waters lifts off the lid from a black box the size of a small laptop. He picks up first one, then another of the 20 or so pre-Clovis stone tools lying inside. Fashioned from a lustrous local chert found near Buttermilk Creek, the blades and other tools are remarkably compact and lightweight, some measuring no more than a few centimeters in length. Such a tool kit, Waters says, would have been ideal for bands of early explorers.

In some of these tools—particularly the blades and bifaces—Waters also sees something else: a new clue to the origins of the Clovis people. Some 2,500 years after the pre-Clovis people here knapped blades and bifaces, Clovis hunters employed similar techniques across North America to make massive elongate blades, some reaching 21 centimeters or more in length. This technological continuity, Waters observes, hints strongly at a relationship between the two groups. Far from being migrants from Asia, the famous Clovis hunters may well have descended from bands such as the earliest hunters at Buttermilk Creek. "It looks as if they originated south of the ice sheet," he remarks.

What is beyond all doubt, however, is that the earliest Americans and their descendants were resourceful trailblazers who peopled the longest geographical expanse ever settled by humans. Braving the unknown, they adapted masterfully to a vast array of ecosystems on two continents. These early Americans deserve our admiration, says archaeologist David Anderson of the University of Tennessee. "I think they exemplify the spirit of survival and adventure that represents the very best of humanity." SA

### MORE TO EXPLORE

**Paleoindian Seafaring, Maritime Technologies, and Coastal Foraging on California's Channel Islands.** Jon M. Erlandson et al. in *Science,* Vol. 331, pages 1181–1185; March 4, 2011.
**The Buttermilk Creek Complex and the Origins of Clovis at the Debra L. Friedkin Site, Texas.** Michael R. Waters et al. in *Science,* Vol. 331, pages 1599–1603; March 25, 2011.
**Constraining the Late Wisconsinan Retreat of the Laurentide Ice Sheet from Western Canada Using Luminescence Ages from Postglacial Aeolian Dunes.** Kennedy Munyikwa et al. in *Quaternary Geochronology,* Vol. 6, No. 4, pages 407–422; June 2011.
Interactive map of Paleo-American sites and possible migration routes can be found at ScientificAmerican.com/nov2011/pringle



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IN BRIEF

**Neandertals,** our closest relatives, ruled Europe and western Asia for more than 200,000 years. But sometime after 28,000 years ago, they vanished.

**Scientists** have long debated what led to their disappearance. The latest extinction theories focus on climate change and subtle differences in behavior and biology that might have given modern humans an advantage over the Neandertals.

PALEOANTHROPOLOGY

# Twilight of the

**Paleoanthropologists know more about Neandertals than any other extinct human. But their demise remains a mystery, one that gets curiouser and curiouser**

BY KATE WONG

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# Neandertals

Some 28,000 years ago in what is now the British territory of Gibraltar, a group of Neandertals eked out a living along the rocky Mediterranean coast. They were quite possibly the last of their kind. Elsewhere in Europe and western Asia, Neandertals had disappeared thousands of years earlier, after having ruled for more than 200,000 years. The Iberian Peninsula, with its comparatively mild climate and rich array of animals and plants, seems to have been the final stronghold. Soon, however, the Gibraltar population, too, would die out, leaving behind only a smattering of their stone tools and the charred remnants of their campfires.

*Illustration by Kazuhiko Sano*



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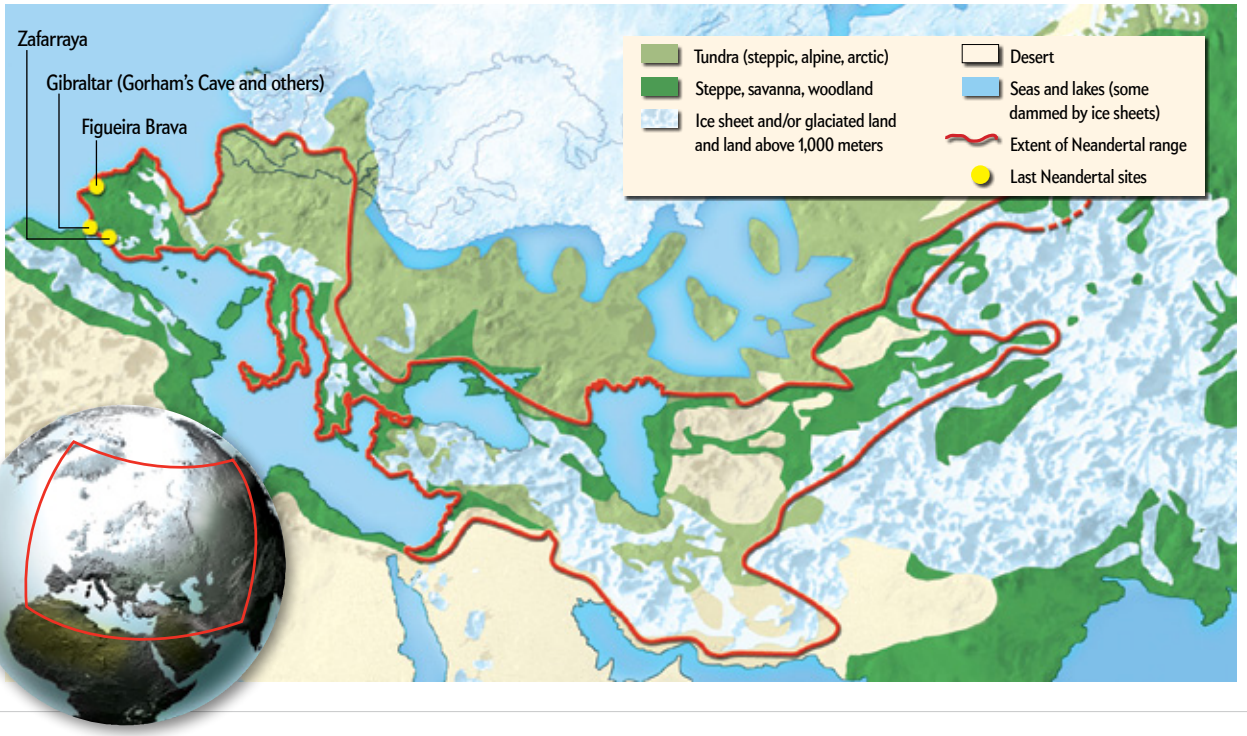
# Did Climate Change Doom the Neandertals?

**Starting perhaps** around 55,000 years ago, climate in Eurasia began to swing wildly from frigid to mild and back again in the span of decades. During the cold snaps, ice sheets advanced and treeless tundra replaced wooded environments across much of the Neandertals' range. Shifts in the available prey animals accompanied these changes. Wide spacing between past climate fluctuations allowed diminished Neandertal populations sufficient time to bounce back and adapt to the new conditions.

This time, however, the rapidity of the changes may have made recovery impossible. By 30,000 years ago only a few pockets of Neandertals survived, hanging on in the Iberian Peninsula, with its comparatively mild climate and rich resources. These groups were too small and fragmented to sustain themselves, however, and eventually they disappeared. The map below shows conditions associated with the last glacial maximum, some 20,000 years ago, which provide an approximation of the extreme conditions Neandertals probably endured toward the end of their reign.


Zafarraya
Gibraltar (Gorham's Cave and others)
Figueira Brava
Tundra (steppic, alpine, arctic)
Steppe, savanna, woodland
Ice sheet and/or glaciated land and land above 1,000 meters
Desert
Seas and lakes (some dammed by ice sheets)
Extent of Neandertal range
Last Neandertal sites

Ever since the discovery of the first Neandertal fossil in 1856, scientists have debated the place of these bygone humans on the family tree and what became of them. Recent analyses of Neandertal DNA indicate that they interbred with modern humans. In addition, improvements in dating methods show that rather than disappearing immediately after the moderns invaded Europe, starting a little more than 40,000 years ago, the Neandertals survived for nearly 15,000 years after moderns moved in. These findings make clear that moderns did not simply extirpate the Neandertals on entering their territory, as one theory envisioned. How, then, did our closest evolutionary relatives become extinct? Mounting evidence suggests that the answer involves a complicated interplay of stresses.

## A WORLD IN FLUX

ONE OF THE MOST INFORMATIVE new lines of evidence bearing on why the Neandertals died out is paleoclimate data. Scholars have known for some time that Neandertals experienced both glacial conditions and milder interglacial conditions during their long reign. In recent years, however, analyses of isotopes trapped in primeval ice, ocean sediments and pollen retrieved from such locales as Greenland, Venezuela and Italy have enabled investigators to reconstruct a far finer-grained picture of the climate shifts that occurred during a period known as oxygen isotope stage 3 (OIS-3). Spanning the time between roughly 65,000 and 25,000 years ago, OIS-3 began with moderate conditions and culminated with the ice sheets blanketing northern Europe.

Considering that Neandertals were the only hominids in Europe at the beginning of OIS-3 and moderns were the only ones there by the end of it, experts have wondered whether the plummeting temperatures might have caused the Neandertals to perish, perhaps because they could not find enough food or keep sufficiently warm. Yet arguing for that scenario has proved tricky for one essential reason: Neandertals had faced glacial conditions before and persevered.

In fact, numerous aspects of Neandertal biology and behavior indicate that they were well suited to the cold. Their barrel chests and stocky limbs would have conserved body heat, although they would have additionally needed clothing fashioned from animal pelts to stave off the chill. And their brawny build seems to have been adapted to their ambush-style hunting of large, relatively solitary mammals—such as woolly rhinoceroses—that roamed north-

SOURCE: "RAPID ECOLOGICAL TURNOVER AND ITS IMPACT ON NEANDERTAL AND OTHER HUMAN POPULATIONS," BY CLIVE FINLAYSON AND JOSÉ S. CARRIÓN, IN *TRENDS IN ECOLOGY AND EVOLUTION*, VOL. 22, NO. 4, 2007



*Map by Laurie Grace*

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ern and central Europe during the cold snaps. (Other distinctive Neandertal features, such as the form of the prominent brow, may have been adaptively neutral traits that became established through genetic drift, rather than selection.)

But the isotope data reveal that far from progressing steadily from mild to frigid, the climate became increasingly unstable heading into the last glacial maximum, swinging severely and abruptly. With that flux came profound ecological change: forests gave way to treeless grassland; reindeer replaced certain kinds of rhinoceroses. So rapid were these oscillations that over the course of an individual's lifetime, all the plants and animals that a person had grown up with could vanish and be replaced with unfamiliar flora and fauna. And then, just as quickly, the environment could change back again.

It is this seesawing of environmental conditions—not necessarily the cold, per se—that gradually pushed Neandertal populations to the point of no return, according to scenarios posited by such experts as evolutionary ecologist Clive Finlayson of the Gibraltar Museum, who directs the excavations at several cave sites in Gibraltar. These shifts would have demanded that Neandertals adopt a new way of life in very short order. For example, the replacement of wooded areas with open grassland would have left ambush hunters without any trees to hide behind, he says. To survive, the Neandertals would have had to alter the way they hunted.

Some Neandertals did adapt to their changing world, as evidenced by shifts in their tool types and prey. But many probably died out during these fluctuations, leaving behind ever more fragmented populations. Under normal circumstances, these archaic humans might have been able to bounce back, as they had previously, when the fluctuations were fewer and farther between. This time, however, the rapidity of the environmental change left insufficient time for recovery. Eventually, Finlayson argues, the repeated climatic insults left the Neandertal populations so diminished that they could no longer sustain themselves.

The results of a genetic study published in 2009 in *PLoS One* by Virginie Fabre and her colleagues at the University of the Mediterranean in Marseille support the notion that Neandertal populations were fragmented, Finlayson says. That analysis of Neandertal mitochondrial DNA found that the Neandertals could be divided into three subgroups—one in western Europe, another in southern Europe and a third in western Asia—and that population size ebbed and flowed.

**A growing body of evidence indicates that Neandertals were savvier than they have been given credit for.**

### INVASIVE SPECIES

FOR OTHER RESEARCHERS, however, the fact that the Neandertals entirely disappeared only after moderns entered Europe clearly indicates that the invaders had a hand in the extinction, even if the newcomers did not kill the earlier settlers outright. Probably, contend those who hold this view, the Neandertals ended up competing with the incoming moderns for food and gradually lost ground. Exactly what ultimately gave modern humans their winning edge remains a matter of considerable disagreement, though.

One possibility is that moderns were less picky about what they ate. Analyses of Neandertal bone chemistry conducted by Hervé Bocherens of the University of Tübingen in Germany suggest that at least some of these hominids specialized in large mammals, such as woolly rhinoceroses, which were relatively rare. Early modern humans, on the other hand, ate all manner of animals and plants. Thus, when moderns moved into Neandertal territory and started taking some of these large animals for themselves, so the argument goes, the Neandertals would have been in trouble. Moderns, meanwhile, could supplement the big kills with smaller animals and an abundance of plant foods. (This is not to say Neandertals never ate veggies. A study published in *Naturwissenschaften* in July 2012 suggests that Neandertals at El Sidrón Cave in Spain ate cooked plants—including medicinal varieties—50,000 years ago.)

"Neandertals had a Neandertal way of doing things, and it was great as long as they weren't competing with moderns," observes archaeologist Curtis W. Marean of Arizona State University. In contrast, Marean says, the moderns, who evolved under tropical conditions in Africa, were able to enter entirely different environments and very quickly come up with creative ways to deal with the novel circumstances they encountered. "The key difference is that Neandertals were just not as advanced cognitively as modern humans," he asserts.

Marean is not alone in thinking that Neandertals were one-trick ponies. A long-standing view holds that moderns outsmart-

*Illustration by Viktor Deak*

## RESURRECTING THE NEANDERTAL

In 2010 Svante Pääbo of the Max Planck Institute for Evolutionary Anthropology in Leipzig published a draft of the Neandertal genome. The work has prompted speculation that scientists might one day be able to bring back this extinct human. Such a feat, if it were technically possible, would raise all sorts of ethical quandaries: What rights would a Neandertal have? Would this individual live in a lab, or a zoo, or a household?

Moral concerns aside, what could researchers actually learn from a resurrected Neandertal? The answer is: less than you might think. A Neandertal born and raised in a modern setting would not have built-in Ice Age wisdom to impart to us, such as how to make a Mousterian stone tool or bring down a woolly rhinoceros. Indeed, he would not be able to tell scholars anything about the culture of his people. It is possible, however, that studying Neandertal biology and cognition could reveal as yet unknown differences between these archaic hominids and modern ones that might have given moderns a survival advantage.



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ed the Neandertals with not only their superior tool technology and survival tactics but also their gift of gab, which might have helped them form stronger social networks. The Neandertal dullards, in this view, did not stand a chance against the newcomers.

But a growing body of evidence indicates that Neandertals were savvier than they have been given credit for. In fact, they apparently engaged in many of the behaviors once believed to be strictly the purview of modern humans. As paleoanthropologist Christopher B. Stringer of London's Natural History Museum puts it, "the boundary between Neandertals and moderns has gotten fuzzier."

Sites in Gibraltar have yielded some of the finds blurring the line between the two human groups. In September 2008 Stringer and his colleagues reported on evidence that Neandertals at Gorham's Cave and next-door Vanguard Cave hunted dolphins and seals as well as gathered shellfish. They ate birds and rabbits, too. The discoveries in Gilbraltar, along with finds from a handful of other sites, upend the received wisdom that moderns alone exploited marine resources and small game.

More evidence blurring the line between Neandertal and modern human behavior has come from the site of Hohle Fels in southwestern Germany. There paleoanthropologist Bruce Hardy of Kenyon College was able to compare artifacts made by Neandertals who inhabited the cave between 36,000 and 40,000 years ago with artifacts from modern humans who resided there between 33,000 and 36,000 years ago under similar climate and environmental conditions. In a presentation given in 2009 to the Paleoanthropology Society in Chicago, Hardy reported that his analysis of the wear patterns on the tools and the residues from substances with which the tools came into contact revealed that although the modern humans created a larger variety of tools than did the Neandertals, the groups engaged in mostly the same activities at Hohle Fels.

These activities include such advanced practices as using tree resin to bind stone points to wooden handles, employing stone points as thrusting or projectile weapons, and crafting implements from bone and wood. As to why the Hohle Fels Neandertals made fewer types of tools than did the moderns who lived there afterward, Hardy surmises that they were able to get the job done without them. "You don't need a grapefruit spoon to eat a grapefruit," he says.

The claim that Neandertals lacked language, too, seems unlikely in light of recent discoveries. Researchers now know that at least some of them decorated their bodies with jewelry and probably pigment. Such physical manifestations of symbolic behavior are often used as a proxy for language when reconstructing behavior from the archaeological record. And in 2007 researchers led by Johannes Krause, now at the University of Tübingen in Germany, reported that analyses of Neandertal DNA have shown that these hominids had the same version of the speech-enabling gene *FOXP2* that modern humans carry.

### TIEBREAKERS

WITH THE GAP between Neandertal and modern human behavior narrowing, many researchers are now looking to subtle differences in culture and biology to explain why the Neandertals lost out. "Worsening and highly unstable climatic conditions would have made competition among human groups all the more fierce," reflects paleoanthropologist Katerina Harvati, also now at Tübingen. "In this context, even small advantages would become extremely important and might spell the difference between survival and death."

Stringer, for his part, theorizes that the moderns' somewhat wider range of cultural adaptations provided a slightly superior buffer against hard times. For example, needles left behind by modern humans hint that they had tailored clothing and tents, all the better for keeping the cold at bay. Neandertals, meanwhile, left behind no such signs of sewing and are believed by some to have had more crudely assembled apparel and shelters as a result.

Neandertals and moderns may have also differed in the way they divvied up the chores among group members. In a paper published in *Current Anthropology* in 2006, archaeologists Steven L. Kuhn and Mary C. Stiner, both at the University of Arizona, hypothesized that the varied diet of early modern Europeans would have favored a division of labor in which men hunted the larger game and women collected and prepared nuts,

HYPOTHESIS 2

## Were the Neandertals Outsmarted by Modern Humans?

**A long-standing theory** of Neandertal extinction holds that modern humans outcompeted Neandertals with their superior smarts. But mounting evidence indicates that Neandertals engaged in many of the same sophisticated behaviors once attributed to moderns alone (*table*). The findings reveal that at least some Neandertals were capable of symbolic thought—and therefore probably language—and that they had the tools and the know-how to pursue a wide range of foods. Still, these practices seem to have been more entrenched in modern human culture than in that of Neandertals, which may have given moderns the upper hand.

### EVIDENCE OF MODERN BEHAVIOR AMONG NEANDERTALS

| TRAIT | Common | Occasional | Absent | Uncertain |
|---|---|---|---|---|
| Art | | | | ● |
| Pigment use | ● | | | |
| Jewelry | | ● | | |
| Symbolic burial of dead | | | | ● |
| Long-distance exchange | | | | ● |
| Microliths | | ● | | |
| Barbed points | | | ● | |
| Bone tools | | ● | | |
| Blades | | ● | | |
| Needles | | | ● | |
| Exploitation of marine resources | | ● | | |
| Bird hunting | | ● | | |
| Division of labor | | | ● | |



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**LAST BASTION of the Neandertals may have been a group of coastal caves in the British territory of Gibraltar, where the archaic hominids lived as recently as 28,000 years ago. Gibraltar and the rest of the Iberian Peninsula would have had a relatively mild climate and abundant food resources compared with much of Ice Age Europe.**

seeds and berries. In contrast, the Neandertal focus on large game probably meant that their women and children joined in the hunt, possibly helping to drive animals toward the waiting men. With the creation of both a more reliable food supply and a safer environment for rearing children, division of labor could have enabled modern human populations to expand at the expense of the Neandertals.

However the Neandertals obtained their food, they needed lots of it. "Neandertals were the SUVs of the hominid world," says paleoanthropologist Leslie Aiello of the Wenner-Gren Foundation in New York City. A number of studies aimed at estimating metabolic rates have concluded that Neandertals required significantly more calories to survive than the rival moderns did.

Hominid energetics expert Karen Steudel-Numbers of the University of Wisconsin–Madison has determined, for example, that the energetic cost of locomotion was 32 percent higher in Neandertals than in anatomically modern humans, thanks to the archaic hominids' burly build and short shinbones, which would have shortened their stride. In terms of daily energy needs, the Neandertals would have required somewhere between 100 and 350 calories more than moderns living in the same climates, according to a model developed by Andrew W. Froehle, now at Wright State University, and Steven E. Churchill of Duke University. Modern humans, then, might have outcompeted Neandertals simply by virtue of being more fuel-efficient.

One more distinction between Neandertals and moderns deserves mention. Research led by Rachel Caspari of Central Michigan University has shown that around 30,000 years ago, the number of modern humans who lived to be old enough to be grandparents began to skyrocket [see Caspari's article on "The Evolution of Grandparents," on page 38]. Exactly what spurred this increase in longevity is uncertain, but it meant that people had more reproductive years and more time over which to acquire specialized knowledge and pass it on to the next generation. "Long-term survivorship gives the potential for bigger social networks and greater knowledge stores," Stringer comments. Among the shorter-lived Neandertals, in contrast, knowledge was more likely to disappear, he surmises.

More clues to why the Neandertals faded away may come from analysis of the Neandertal genome. Scientists know little about the functional significance of most regions of the modern genome, never mind the Neandertal one, but future analyses could conceivably pinpoint cognitive or metabolic differences between the two groups and reveal how extensively they interbred.

The Stone Age whodunit is far from solved. But researchers are converging on one conclusion: regardless of whether climate or competition with moderns, or some combination thereof, was the prime mover in the decline of the Neandertals, the precise factors governing the extinction of individual populations of these archaic hominids almost certainly varied from group to group. Some may have perished from disease, others from inbreeding. "Each valley may tell its own story," Finlayson remarks.

As for the last known Neandertals, the ones who lived in Gibraltar's seaside caves some 28,000 years ago, Finlayson is certain that they did not spend their days competing with moderns, because moderns seem not to have settled there until thousands of years after the Neandertals were gone. The rest of their story, however, remains to be discovered. SA

**KATE WONG** is a senior editor at *Scientific American*.

MORE TO EXPLORE

**The Humans Who Went Extinct: Why Neanderthals Died Out and We Survived.** Clive Finlayson. Oxford University Press, 2009.

**A Draft Sequence of the Neandertal Genome.** Richard E. Green et al. in *Science*, Vol. 328, pages 710–722; May 7, 2010.

**Lone Survivors: How We Came to Be the Only Humans on Earth.** Chris Stringer. Times Books, 2012.

NATURAL HISTORY MUSEUM, LONDON (caves)

*Map by Laurie Grace*



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GENETICS

# Our Inner Neandertal

## Genome analysis indicates Neandertals and modern humans interbred

BY KATE WONG

**FRIENDS AND LOVERS?** DNA analysis shows that anatomically modern humans (*left*) mated with Neandertals (*right*). They also interbred with other archaic humans, such as *Homo erectus*.

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**UP TO 4 PERCENT OF THE DNA OF PEOPLE TODAY** who live outside Africa came from Neandertals, the result of interbreeding between Neandertals and early modern humans. That conclusion comes from scientists led by Svante Pääbo of the Max Planck Institute for Evolutionary Anthropology in Leipzig, who pieced together the first draft of the Neandertal genome—which represents about 60 percent of the entire genome—using DNA obtained from three Neandertal bones that come from Vindija Cave in Croatia and are more than 38,000 years old.

The evidence that Neandertals contributed DNA to modern humans came as a shock to the investigators, who published their findings in the May 7, 2010, *Science* issue. "First I thought it was some kind of statistical fluke," Pääbo remarked during a press teleconference. The finding contrasts sharply with his previous work. In 1997 he and his colleagues sequenced the first Neandertal mitochondrial DNA. Mitochondria are the cell's energy-generating organelles, and they have their own DNA, which is distinct from the much longer DNA sequence that resides in the cell's nucleus. Their analysis revealed that Neandertals had not made any contributions to modern mitochondrial DNA. Yet because mitochondrial DNA represents only a tiny fraction of an individual's genetic makeup, the possibility remained that Neandertal nuclear DNA might tell a different story. Still, additional genetic analyses have typically led researchers to conclude that *Homo sapiens* arose in Africa and replaced the archaic humans it encountered as it spread out from its birthplace without mingling with them—the out of Africa replacement scenario, as it is known.

But mingle they apparently did. When Pääbo's team looked at patterns of nuclear genome variation in present-day humans, it identified 12 genome regions where non-Africans exhibited variants that were not seen in Africans and that were thus candidates for being derived from the Neandertals, who lived not in Africa but Eurasia. Comparing those regions with the same regions in the Neandertal sequence, the researchers found that 10 of these 12 variants in non-Africans came from Neandertals. The contributions did not seem to encode anything of functional importance, although subsequent analysis has hinted that Neandertals may have passed along disease-fighting genes.

Intriguingly, the researchers failed to detect a special affinity to Europeans—a link that might have been expected given that Neandertals seem to have persisted in Europe longer than anywhere else before disappearing around 28,000 years ago. Rather the Neandertal sequence was equally close to sequences from present-day people from France, Papua New Guinea and China. By way of explanation, the investigators suggest that the interbreeding occurred in the Middle East between 50,000 and 80,000 years ago, before moderns fanned out to other parts of the Old World and split into different groups.

Intermixing does not surprise paleoanthropologists who have long argued on the basis of fossils that archaic humans, such as the Neandertals in Eurasia and *Homo erectus* in East Asia, mated with early moderns and can be counted among our ancestors—the so-called multiregional evolution theory of modern human origins. The detection of Neandertal DNA in present-day people thus comes as welcome news to these scientists. "It is important evidence for multiregional evolution," comments Milford H. Wolpoff of the University of Michigan, the leading proponent of the theory.

**"This is just the beginning of the exploration of human uniqueness that is now possible."**
**—Svante Pääbo**

In a prepared statement, out of Africa theorist Christopher B. Stringer of the Natural History Museum in London acknowledged that the genome results show that "many of us outside of Africa have some [Neandertal] inheritance." But Stringer maintains that the origin of our species is mostly an out of Africa story. Population geneticist Laurent Excoffier of the University of Bern in Switzerland agrees, noting that the alleged admixture did not continue as moderns moved into Europe. "In all scenarios of speciation, there is a time during which two diverging species remain interfertile," he explains.

In addition to illuminating how early humans interacted, the Neandertal genome is helping to indicate which parts of the modern human genome separate us from all other creatures. Thus far Pääbo's group has identified a number of modern human genome regions containing sequence variation that is not seen in Neandertals and that may have helped modern humans adapt. Some of these regions are involved in cognitive development, sperm movement and the physiology of the skin.

Exactly how these slight changes to the modern human sequence affected the functioning of these genome regions remains to be determined. Says Pääbo: "This is just the beginning of the exploration of human uniqueness that is now possible." SA

**KATE WONG** is a senior editor at *Scientific American*.

MORE TO EXPLORE

**A Draft Sequence of the Neandertal Genome.** Richard E. Green et al. in *Science*, Vol. 328, pages 710–722; May 7, 2010.
**Drafting Human Ancestry: What Does the Neanderthal Genome Tell Us about Hominid Evolution? Commentary on Green et al. (2010).** Michael Hofreiter in *Human Biology*, Vol. 83, No. 1, pages 1–11; February 2011.

E. R. DEGGINGER *Photo Researchers, Inc. (human and Neandertal skulls)*



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PALEOANTHROPOLOGY

# Rethinking the Hobbits of Indonesia

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**STRANGE SKELETON** from Flores, Indonesia, calls into question which human ancestor was the first to leave Africa—and when. Archaeologist Thomas Sutikna (*left*) is one of the leaders of the excavation of the cave that yielded the skeleton.

The mini human species found in Indonesia turns out to be even stranger than previously thought and complicates the story of our ancient past

BY KATE WONG

PHOTOGRAPHS BY DJUNA IVEREIGH

In 2004 a team of Australian and Indonesian scientists who had been excavating a cave called Liang Bua on the Indonesian island of Flores announced that they had unearthed something extraordinary: a partial skeleton of an adult human female who would have stood just over a meter tall and who had a brain a third as large as our own. The specimen, known to scientists as LB1, quickly received a fanciful nickname—the hobbit, after writer J.R.R. Tolkien's fictional creatures. The researchers proposed that LB1 and the other fragmentary remains they recovered represent a previously unknown human species, *Homo floresiensis*. Their best guess was that *H. floresiensis* was a descendant of *Homo erectus*—the first species known to have colonized outside of Africa. The creature evolved its small size, they surmised, as a response to the limited resources available on its island home—a phenomenon that had previously been documented in other mammals, but never humans.

The finding jolted the paleoanthropological community. Not only was *H. floresiensis* being held up as the first example of a human following the so-called island rule, but it also seemed to reverse a trend toward ever larger brain size over the course of human evolution. Furthermore, the same deposits in which the small-bodied, small-brained individuals were found also yielded stone tools for hunting and butchering animals, as well as remainders of fires for cooking them—rather advanced behaviors for a creature with a brain the size of a chimpanzee's. And astonishingly, LB1 lived just 18,000 years ago—thousands of years after our other late-surviving relatives, the Neandertals and *H. erectus,* disappeared.

Skeptics were quick to dismiss LB1 as nothing more than a modern human with a disease that stunted her growth. And since the announcement of the discovery, they have proposed a number of possible conditions to explain the specimen's peculiar features, from cretinism to Laron syndrome, a genetic disease that causes insensitivity to growth hormone. Their arguments have failed to convince the hobbit proponents, however, who have countered each diagnosis with evidence to the contrary.

## A PERPLEXING PASTICHE

Nevertheless, recent analyses are causing even the proponents to rethink important aspects of the original interpretation of the discovery. The findings are also forcing paleoanthropologists to reconsider established views of such watershed moments in human evolution as the initial migration out of Africa by hominins (the group that includes all the creatures in the human line since it branched away from chimpanzees).

Perhaps the most startling realization to emerge from the latest studies is how very primitive LB1's body is in many respects. (To date, excavators have recovered the bones of some

### IN BRIEF

**In 2004** researchers working on the island of Flores in Indonesia found bones of a miniature human species—formally named *Homo floresiensis* and nicknamed the hobbit—that lived as recently as 17,000 years ago.

**Scientists** initially postulated that *H. floresiensis* descended from *Homo erectus,* a human ancestor with body proportions similar to our own.

**New investigations** show that the hobbits were more primitive than researchers thought, however—a finding that could overturn key assumptions about human evolution.



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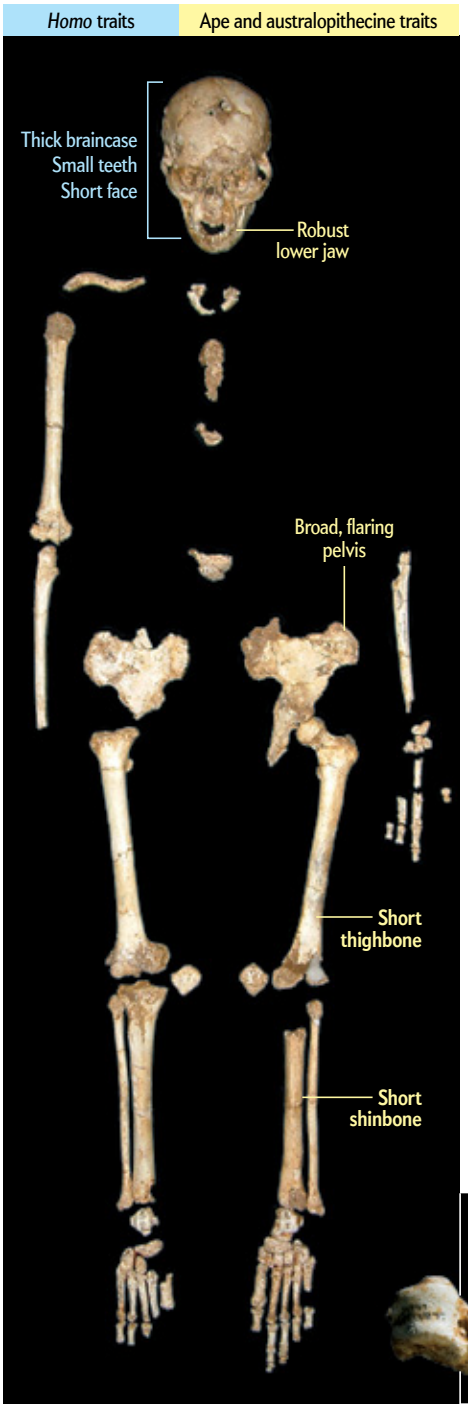
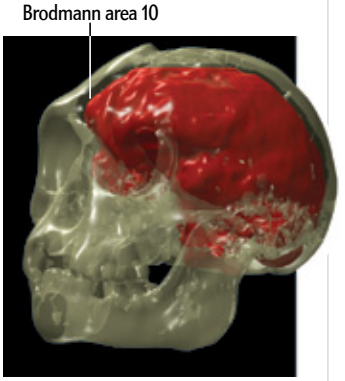
# A Mysterious Mosaic

**To date,** excavators have recovered the remains of about 14 individuals from Liang Bua, a cave site on Flores. The most complete specimen is a nearly complete skeleton called LB1 that dates to 18,000 years ago. Some of its characteristics call to mind those of apes and of australopithecines such as the 3.2-million-year-old Lucy. Other traits, however, are in keeping with those of our own genus, *Homo*. This mélange of primitive features (*yellow*) and modern ones (*blue*) has made it difficult to figure out where on the human family tree the hobbits belong.




**BRAIN** is the size of a chimpanzee's. But a virtual reconstruction—generated from CT scans of the interior of the braincase—indicates that despite its small size, the organ had a number of advanced features, including an enlarged Brodmann area 10, a part of the brain that has been theorized to play a role in complex cognitive activities. Such features may help explain how a creature with a brain the size of a chimp's was able to make stone tools.

**WRIST** resembles that of an African ape. Of particular interest is a bone called the trapezoid, which has a pyramidal form. Modern humans, in contrast, have a trapezoid shaped like a boot, which facilitates tool manufacture and use by better distributing forces across the hand.

**FOOT** is exceptionally long compared with the short leg. This relative foot length is comparable to that seen in bonobos, and it suggests the hobbits were inefficient runners. Other apelike traits include long, curved toes and the absence of an arch (*below*). Yet the big toe aligns with the rest of the toes, among other modern characteristics.

14 individuals from the site, but LB1 remains the most complete specimen by far.) From the outset, the specimen has invited comparisons to the 3.2-million-year-old Lucy—the best-known representative of a human ancestor called *Australopithecus afarensis*—because they were about the same height and had similarly small brains. But it turns out LB1 has much more than size in common with Lucy and other pre-*erectus* hominins. And a number of her features are downright apelike.

A particularly striking example of the bizarre morphology of the hobbits surfaced in May 2009, when researchers led by William L. Jungers of Stony Brook University published their analysis of LB1's foot. The foot has a few modern features—for instance, the big toe is aligned with the other toes, as opposed to splaying out to the side as it does in apes and australopithecines. But by and large, it is old-fashioned. Measuring around 20 centimeters in length, LB1's foot is 70 percent as long as her short thighbone, a ratio unheard of for a member of the human family. The foot of a modern human, in contrast, is on average 55 percent as long as the femur. The closest match to LB1 in this regard, aside from, perhaps, the large-footed hobbits of Tolkien's imagination, is a bonobo. Furthermore, LB1's big toe is short, her other toes are long and slightly curved, and her foot lacks a proper arch—all primitive traits.

"A foot like this one has never been seen before in the human fossil record," Jungers said in a statement to the press. Characteristics of the pelvis, leg and foot make clear that the hobbits walked upright. But with their short legs and relatively long feet, they would have had to use a high-stepping gait to avoid dragging their toes on the ground. Thus, although they could probably sprint short distances—say, to avoid becoming dinner for one of the Komodo dragons that patrolled Flores—they would not have won any marathons.

If the foot were the only part of the hobbit to exhibit such primitive traits, scientists might have an easier time upholding the idea that *H. floresiensis* is a dwarfed descendant of *H. erectus* and just chalking the foot morphology up to an evolutionary reversal that occurred as a consequence of dwarfing. But the fact is that archaic features are found throughout the entire skeleton of LB1. A bone in the wrist called the trape-

COURTESY OF WILLIAM L. JUNGERS *Stony Brook University (skeleton);*
COURTESY OF KIRK E. SMITH *Mallinckrodt Institute of Radiology, Washington University School of Medicine in St. Louis (skull)*



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zoid, which in our own species is shaped like a boot, is instead shaped like a pyramid, as it is in apes; the clavicle is short and quite curved, in contrast to the longer, straighter clavicle that occurs in hominins of modern body form; the pelvis is basin-shaped, as in australopithecines, rather than funnel-shaped, as in *H. erectus* and other later *Homo* species. The list goes on.

Indeed, from the neck down LB1 looks more like Lucy and the other australopithecines than *Homo*. But then there is the complicated matter of her skull. Although it encased a grapefruit-size brain measuring just 417 cubic centimeters—a volume within the range of chimpanzees and australopithecines—other cranial features, such as the narrow nose, mark LB1 as a member of our genus, *Homo*.

## PRIMITIVE ROOTS

FOSSILS THAT COMBINE *Homo*-like skull characteristics with primitive traits in the trunk and limbs are not unprecedented. The earliest members of our genus, such as *Homo habilis,* also exhibit a hodgepodge of old and new. Thus, as details of the hobbits' postcranial skeletons have emerged, researchers have increasingly wondered whether the little Floresians might belong to a primitive *Homo* species, rather than having descended from *H. erectus,* which had modern body proportions.

An analysis conducted by Debbie Argue of the Australian National University in Canberra and her colleagues bolsters this view. To tackle the problem of how the hobbits are related to other members of the human family, the team employed cladistics—a method that looks at shared, novel traits to work out relationships among organisms—comparing anatomical characteristics of LB1 with those of other members of the human family, as well as apes.

In a 2009 paper in the *Journal of Human Evolution,* Argue and her collaborators reported that their results suggest two possible positions for the *H. floresiensis* branch of the hominin family tree. The first position is that *H. floresiensis* evolved after a hominin called *Homo rudolfensis,* which arose some 2.3 million years ago but before *H. habilis,* which appeared roughly two million years ago. The second position is that it emerged after *H. habilis* but still well before *H. erectus,* which arose around 1.8 million years ago. More important, Argue's team found no support for a close relationship between *H. floresiensis* and *H. erectus,* thereby dealing a blow to the theory that the hobbits were the product of island dwarfing of *H. erectus.* (The study also rejected the hypothesis that hobbits belong to our own species.)

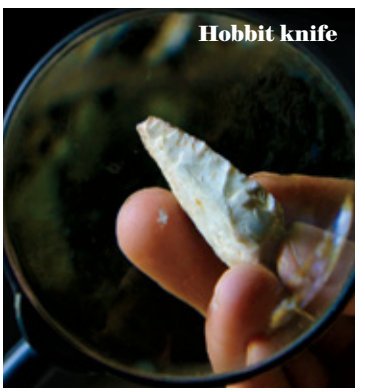
If the hobbits are a very early species of *Homo* that predates *H. erectus,* that positioning on the family tree would go a long way toward accounting for LB1's tiny brain, because the earliest members of our genus had significantly less gray matter than the average *H. erectus* possessed. But Argue's findings do not solve the brain problem entirely. LB1 aside, the smallest known noggin in the genus *Homo* is an *H. habilis* specimen with an estimated cranial capacity of 509 cubic centimeters. LB1's brain was some 20 percent smaller than that.

Could island dwarfing still have played a role in determining the size of the hobbit's brain? When the discovery team first attributed LB1's wee brain to this phenomenon, critics complained that her brain was far smaller than it should be for a hominin of her body size, based on known scaling relationships. Mammals that undergo dwarfing typically exhibit only moderate reduction in brain size. But dwarfing of mammals on islands may present a special case. Eleanor Weston and Adrian Lister of the Natural History Museum in London found that in several species of fossil hippopotamus that became dwarfed on the African island nation of Madagascar, brain size shrank significantly more than predicted by standard scaling models. Based on their hippo model, the study authors contend, even an ancestor the size of *H. erectus* could conceivably attain the brain and body proportions of LB1 through island dwarfing.

The work on hippos has impressed researchers such as Harvard University's Daniel Lieberman. In a commentary accompanying Weston and Lister's report in *Nature,* Lieberman wrote that their findings "come to the rescue" in terms of explaining how *H. floresiensis* came by such a small brain.

Although some specialists favor the original interpretation of the hobbits, Mike Morwood of the University of Wollongong in Australia, who helps to coordinate the Liang Bua project, now thinks the ancestors of LB1 and the gang were early members of *Homo* who were already small—much smaller than even the tiniest known *H. erectus* individuals—when they arrived on Flores and then "maybe underwent a little insular dwarfing" once they got there.

Artifacts left behind by the hobbits support the claim that *H. floresiensis* is a very primitive hominin. Early reports on the initial discovery focused on the few stone tools found in the hobbit levels at Liang Bua that were surprisingly sophisticated for a such a small-brained creature—an observation that skeptics highlighted to support their contention that the hobbits were modern humans, not a new species. But subsequent analyses led by Mark W. Moore of the University of New England in Australia and Adam R. Brumm, now at the University of Wollongong, have revealed the hobbit toolkit to be overall quite basic and in line with the implements produced by other small-brained hominins. The advanced appearance of a handful of the hobbit tools at Liang Bua, Moore and Brumm concluded, was produced by chance, which


Hobbit knife

## DID *HOMO SAPIENS* COPY HOBBITS?

Analysis of hobbit implements spanning the time from 95,000 to 17,000 years ago indicates that the tiny toolmakers used the same so-called Oldowan techniques that human ancestors in Africa employed nearly two million years ago. The hobbits combined these techniques in distinctive ways, however—a tradition that the modern humans who inhabited Liang Bua starting 11,000 years ago followed, too. This finding raises the intriguing possibility that the two species made contact and that *H. sapiens* copied the hobbits' style of tool manufacture, rather than the other way around.



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# Digging for Hobbits

Liang Bua (*right*) is a large limestone cave located in the lush highlands of western Flores. Beyond the remains of some 14 hobbits, excavations there have yielded thousands of stone tools, as well as the bones of Komodo dragons, elephantlike stegodonts, giant rats and a carnivorous stork that stood nearly two meters high. The hobbits seem to have occupied the cave from around 100,000 to 17,000 years ago, They may have been drawn to Liang Bua because of its proximity to the Wae Racang River, which would have attracted thirsty prey animals. Researchers are now looking for clues to why, after persisting for so long, the hobbits eventually vanished. They are also eager to recover a second small skull. Such a find would establish that LB1 and the other specimens do indeed represent a new species and are not just the remains of diseased modern humans. Bones and teeth containing DNA suitable for analysis would be likewise informative.

**INSIDE THE PIT** team members carefully scrape away dirt layer by layer, exposing bones and artifacts as they go. They record the position of each item of interest before placing it into a plastic bag. Meanwhile the dirt itself is loaded into buckets that are sent up to the surface for closer inspection.

**SEDIMENT REMOVED** from the excavation pit is thoroughly examined for bone and artifact fragments that might have gone unnoticed in the pit. The local Manggarai villagers who work at the site sort through the sediment in three stages: first with their hands (*shown below*), then by sieving the dry sediment through screens, and last by taking the sediment bucket by bucket out to a station set up in the rice paddy outside the cave and wetting the contents before sieving them again, in hopes of recovering even the tiniest teeth and shards of bone.

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**EXCAVATOR** examines a *Stegodon* rib. The concentration of stone tools in this spot indicates that the hobbits butchered the creature here.

is not unexpected considering that the hobbits manufactured thousands of implements.

To make their tools, the hobbits removed large flakes from rocks outside the cave and then struck smaller flakes off the large flakes inside the cave, employing the same simple stone-working techniques favored by humans at another site on Flores 50 kilometers east of Liang Bua called Mata Menge 880,000 years ago—long before modern humans showed up on the island. (The identity of the Mata Menge toolmakers is unknown because no human remains have turned up there yet, but they conceivably could be the ancestors of the diminutive residents of Liang Bua.) Furthermore, the Liang Bua and Mata Menge tools bear a striking resemblance to artifacts from Olduvai Gorge in Tanzania that date to between 1.2 million and 1.9 million years ago and were probably manufactured by *H. habilis*.

### TINY TRAILBLAZER

IN SOME WAYS, the latest theory about the enigmatic Flores bones is even more revolutionary than the original claim. "The possibility that a very primitive member of the genus *Homo* left Africa, perhaps roughly two million years ago, and that a descendant population persisted until only several thousand years ago, is one of the more provocative hypotheses to have emerged in paleoanthropology during the past few years," reflects David S. Strait of the University at Albany S.U.N.Y. Scientists have long believed that *H. erectus* was the first member of the human family to march out of the natal continent and colonize new lands because that is the hominin whose remains appear outside of Africa earliest in the fossil record. In explanation, it was proposed that humans needed to evolve large brains and long striding limbs and to invent sophisticated technology before they could finally leave their homeland.

Today the oldest unequivocal evidence of humans outside of Africa comes from the Republic of Georgia, where researchers have recovered *H. erectus* remains dating to 1.78 million years ago. The discovery of the Georgian remains dispelled that notion of a brawny trailblazer with a tricked-out toolkit because they were on the small side for *H. erectus,* and they made Oldowan tools, rather than the advanced, so-called Acheulean implements experts expected the first pioneers to make. Nevertheless, they were *H. erectus*.

But if proponents of the new view of hobbits are right, the

## SICK HUMAN HYPOTHESES

**Scientists who doubt** that LB1 belongs to a new human species argue that she is simply a modern human with a disease resulting in a small body and small brain. Those who think LB1 does represent a new species, however, have presented anatomical evidence against each of the proposed diagnoses, a few of which are listed below.

**Laron syndrome,** a genetic disease that causes insensitivity to growth hormone.

**Myxoedematous endemic cretinism,** a condition that arises from prenatal nutritional deficiencies that hinder the thyroid.

**Microcephalic osteodysplastic primordial dwarfism type II,** a genetic disorder whose victims have small bodies and small brains but nearly normal intelligence.



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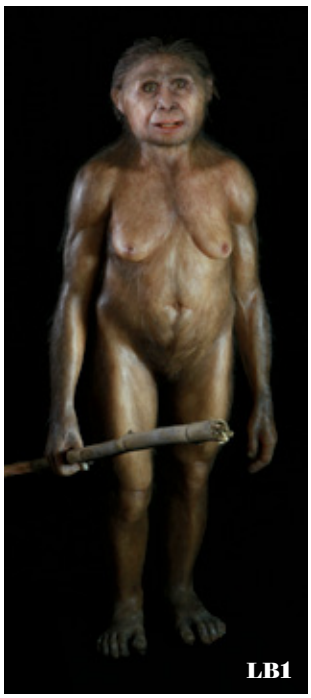
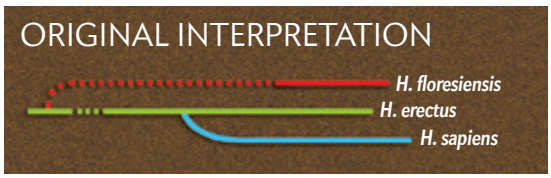
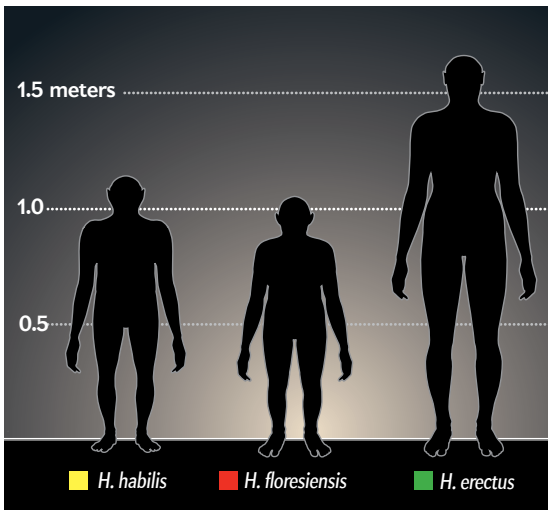
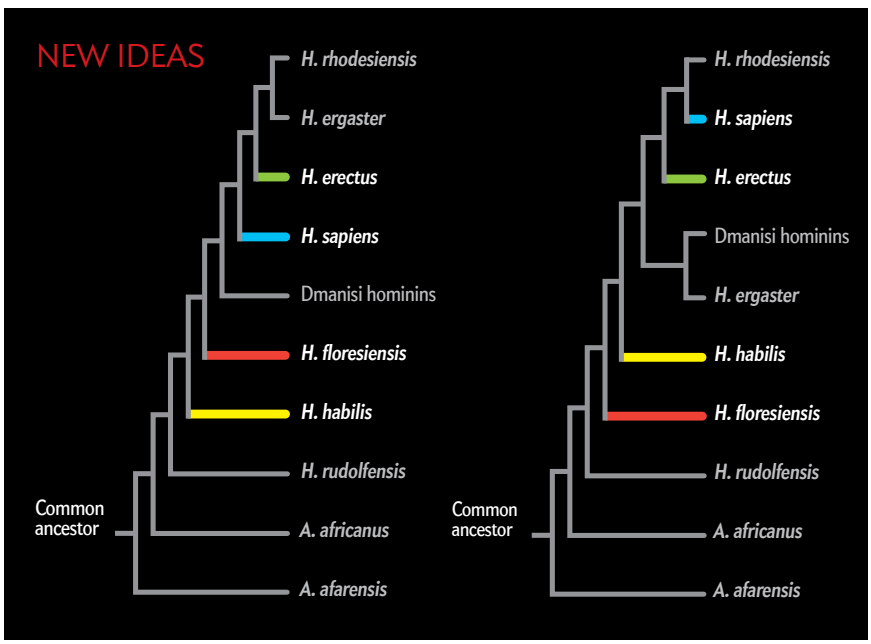
# The Hobbits' Roots

**Researchers** originally believed that LB1 (*left*) and the other hobbits, formally known as *Homo floresiensis,* were descendants of a human ancestor with essentially modern body proportions known as *Homo erectus* that shrank dramatically in response to the limited resources available on their island home. But a recent analysis suggests *H. floresiensis* is significantly more primitive than *H. erectus* and evolved either right after one of the earliest known members of our genus, *Homo habilis* (*bottom left tree*) or right before it (*bottom right tree*). Either way, the study implies that *H. floresiensis* evolved in Africa, along with the other early *Homo* species, and was already fairly small when the species reached Flores, although it may have undergone some dwarfing when it got there.




first intercontinental migrations were undertaken hundreds of thousands of years earlier than that—and by a fundamentally different kind of human, one that arguably had more in common with primitive little Lucy than the colonizer paleoanthropologists had envisioned. This scenario implies that scientists might locate a long-lost chapter of human prehistory in the form of a two-million-year record of this pioneer stretching between Africa and Southeast Asia if they look in the right places.

This suggestion does not sit well with some researchers. "The further back we try to push the divergence of the Flores [hominin], the more difficult it becomes to explain why a [hominin] lineage that must have originated in Africa has left only one trace on the tiny island of Flores," comments primate evolution expert Robert Martin of the Field Museum in Chicago. Martin is unconvinced that *H. floresiensis* is a legitimate new species. In his view, the possibility that LB1—the only hobbit whose brain size is known—was a modern human with an as yet unidentified disorder that gave rise to a small brain has not been ruled out. The question is whether such a condition can also explain the australopithecinelike body of LB1.

Many scientists are welcoming the shake-up. LB1 is "a hominin that no one would be saying anything about if we found it in Africa two million years ago," asserts Matthew W. Tocheri of the Smithsonian Institution, who has analyzed the wrist bones of the hobbits. "The problem is that we're finding it in Indonesia in essentially modern times." The good news, he adds, is that it suggests more such finds remain to be recovered.

"Given how little we know about the Asian hominin record, there is plenty of room for surprises," observes Robin W. Dennell of the University of Sheffield in England. Dennell has postulat-

© 2009 SÉBASTIEN PLAILLY *Look at Sciences (photograph of reconstruction);* ATELIER DAYNES, PARIS *(reconstruction);* CATHERINE WILSON *(height chart);* BASED ON "*HOMO FLORESIENSIS*: A CLADISTIC ANALYSIS," BY DEBBIE ARGUE ET AL., IN *JOURNAL OF HUMAN EVOLUTION,* VOL. 57, NO. 5; NOVEMBER 2009 *(trees)*



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# Blazing a Trail

**The textbook account** of human origins holds that *H. erectus* was the first human ancestor to wander out of Africa and colonize distant lands around 1.8 million years ago. But the evidence from Flores suggests that an older, more primitive forebearer was the original pioneer, one who ventured away from the natal continent perhaps around two million years ago. If so, then paleoanthropologists may have missed a significant chunk of the human fossil record spanning nearly two million years and stretching from Africa to Southeast Asia.

Hobbit hunter Mike Morwood (*below*) is looking for more remains of *H. floresiensis* and its ancestors at two sites on Sulawesi. And he thinks further excavation at Niah Cave in north Borneo could produce evidence of hominins much older than the ones at Liang Bua. The mainland will be harder to comb because rocks of the right age are rarely exposed there.

ed that even the australopithecines might have left Africa, because the grasslands they had colonized in Africa by three million years ago extended into Asia. "What we need, of course, are more discoveries—from Flores, neighboring islands such as Sulawesi, mainland Southeast Asia or anywhere else in Asia," he says.

Morwood, for his part, is attempting to do just that. In addition to the work at Liang Bua and the Soa Basin of central Flores, he is helping to coordinate two projects on Sulawesi. He is eyeing Borneo, too. Searching the mainland for the ancestors of the Liang Bua hobbits will be difficult, however, because rocks of the right age are rarely exposed in this part of the world. But with stakes this high, such challenges are unlikely to prevent intrepid fossil hunters from trying. "If we don't find something in the next 15 years or so in that part of the world, I might start wondering whether we got this wrong," Tocheri reflects. "The predictions are that we should find a whole bunch more." SA

CATHERINE WILSON (*map*)

**KATE WONG** is a senior editor at *Scientific American*.

## MORE TO EXPLORE

**The Primitive Wrist of *Homo floresiensis* and Its Implications for Hominin Evolution.** Matthew W. Tocheri et al. in *Science*, Vol. 317, pages 1743–1745; September 21, 2007.

**A New Human: The Startling Discovery and Strange Story of the "Hobbits" of Flores, Indonesia.** Mike Morwood and Penny van Oosterzee. Smithsonian, 2007.

**The Foot of *Homo floresiensis*.** W. L. Jungers et al. in *Nature*, Vol. 459, pages 81–84; May 7, 2009.

***Homo floresiensis*: A Cladistic Analysis.** Debbie Argue et al. in *Journal of Human Evolution*, Vol. 57, pages 623-639; November 2009.

***Homo floresiensis* and the African Oldowan.** Mark W. Moore and Adam R. Brumm in *Interdisciplinary Approaches to the Oldowan*. Edited by Erella Hovers and David R. Braun. Springer, 2009.

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HUMAN BEHAVIOR

# WHY WE HELP

Far from being a nagging exception to the rule of evolution, cooperation has been one of its primary architects

BY MARTIN A. NOWAK



*Illustration by Noma Bar*

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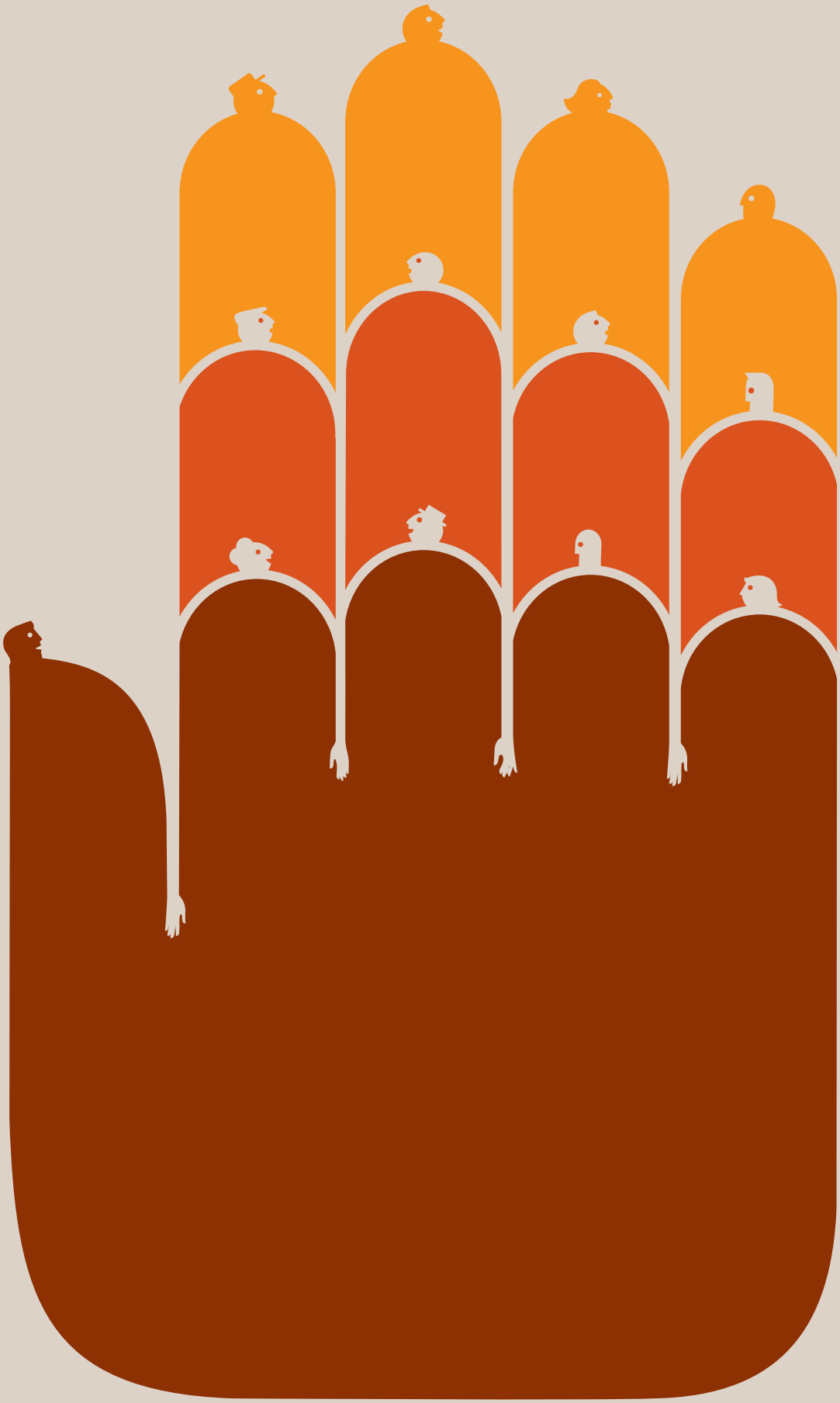

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In April 2011, as reactors at Japan's Fukushima Daiichi nuclear power plant were melting down following a lethal earthquake and tsunami, a maintenance worker in his 20s was among those who volunteered to reenter the plant to try to help bring things back under control. He knew the air was poisoned and expected the choice would keep him from ever marrying or having children for fear of burdening them with health consequences. Yet he still walked back through Fukushima's gates into the plant's radiation-infused air and got to work—for no more compensation than his usual modest wages. "There are only some of us who can do this job," the worker, who wished to remain anonymous, told the *Independent* later, in July. "I'm single and young, and I feel it's my duty to help settle this problem."

Although they may not always play out on such an epic scale, examples of selfless behavior abound in nature. Cells within an organism coordinate to keep their division in check and avoid causing cancer, worker ants in many species sacrifice their own fecundity to serve their queen and colony, female lions within a pride will suckle one another's young. And humans help other humans to do everything from obtaining food to finding mates to defending territory. Even if the helpers may not necessarily be putting their lives on the line, they are risking lowering their own reproductive success for the benefit of another individual.

For decades biologists have fretted over cooperation, scrambling to make sense of it in light of the dominant view of evolution as "red in tooth and claw," as Alfred, Lord Tennyson so vividly described it. Charles Darwin, in making his case for evolution by natural selection—wherein individuals with desirable traits reproduce more often than their peers and thus contribute more to the next generation—called this competition the "struggle for life most severe." Taken to its logical extreme, the argument quickly leads to the conclusion that one should never ever help a rival and that an individual might in fact do well to lie and cheat to get ahead. Winning the game of life—by hook or by crook—is all that matters.

Why, then, is selfless behavior such a pervasive phenomenon? Over the past two decades I have been using the tools of game theory to study this apparent paradox. My work indicates that instead of opposing competition, cooperation has operated alongside it from the get-go to shape the evolution of life on earth, from the first cells to *Homo sapiens*. Life is therefore not just a struggle for survival—it is also, one might say, a snuggle for survival. And in no case has the evolutionary influence of cooperation been more profoundly felt than in humans. My findings hint at why this should be the case and underscore that just as helping one another was the key to our success in the past, so, too, is it poised to be vital to our future.

## FROM ADVERSARY TO ALLY

I first became interested in cooperation back in 1987, as a graduate student studying mathematics and biology at the University of Vienna. While on a retreat with some fellow students and professors in the Alps, I learned about a game theory paradox called the Prisoner's Dilemma that elegantly illustrates why cooperation has so flummoxed evolutionary biologists. The dilemma goes like this: Imagine that two people have been arrested and are facing jail sentences for having conspired to commit a crime. The prosecutor questions each one privately and lays out the terms of a deal. If one person rats on the other and the other remains silent, the incriminator gets just one year of jail time, whereas the silent person gets slammed with a four-year sentence. If both parties cooperate and do not rat on each other, both get reduced sentences of two years. But if both individuals incriminate each other, they both receive three-year sentences.

Because each convict is consulted separately, neither knows whether his or her partner will defect or cooperate. Plotting the possible outcomes on a payoff matrix [*see box on opposite page*], one can see that from an individual's standpoint, the best bet is to defect and incriminate one's partner. Yet because both parties will follow that same line of reasoning and choose defection, both will receive the third-best outcome (three-year sentences) instead of the two-year sentences they could get by cooperating with each other.

The Prisoner's Dilemma seduced me immediately with its power to probe the relation between conflict and cooperation. Eventually my Ph.D. adviser, Karl Sigmund, and I developed techniques to run computer simulations of the dilemma using large communities rather than limiting ourselves to two prisoners. Taking these approaches, we could watch as the strategies of the individuals in these communities evolved from defection to cooperation and back to defection through cycles of growth and decline. Through the simulations, we identified a mechanism that could overcome natural selection's predilection

### IN BRIEF

**People tend to think** of evolution as a strictly dog-eat-dog struggle for survival. In fact, cooperation has been a driving force in evolution.

**There are five mechanisms** by which cooperation may arise in organisms ranging from bacteria to human beings.

**Humans are especially helpful** because of the mechanism of indirect reciprocity, which is based on reputation and leads us to help those who help others.



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for selfish behavior, leading would-be defectors to instead lend helping hands.

We started with a random distribution of defectors and cooperators, and after each round of the game the winners would go on to produce offspring who would participate in the next round. The offspring mostly followed their parents' strategy, although random mutations could shift their strategy. As the simulation ran, we found that within just a few generations all the individuals in the population were defecting in every round of the game. Then, after some time, a new strategy suddenly emerged: players would start by cooperating and then mirror their opponents' moves, tit for tat. The change quickly led to communities dominated by cooperators.

This mechanism for the evolution of cooperation among individuals who encounter one another repeatedly is known as direct reciprocity. Vampire bats offer a striking example. If a bat misses a chance to feed directly on prey one day, it will beg from its sated peers back at the roost. If it is lucky, one of its roost mates will share its blood meal by regurgitating it into the hungry bat's mouth. The vampires live in stable groups and return to the roost every day after hunting, so group members routinely encounter one another. Studies have shown that the bats remember which bats have helped them in times of need, and when the day comes that the generous bat finds itself in need of food, the bat it helped earlier is likely to return the favor.

What made our early computer simulations even more interesting was the revelation that there are different kinds of direct reciprocity. Within 20 generations the initial tit-for-tat strategy had given way to a more generous strategy in which players might still cooperate even if their rival defected. We had, in essence, witnessed the evolution of forgiveness—a direct-reciprocity strategy that allows players to overlook the occasional mistake.

In addition to direct reciprocity, I later identified four more mechanisms for the evolution of cooperation. In the several thousand papers scientists have published on how cooperators could prevail in evolution, all the scenarios they describe fall into one or more of these five categories.

A second means by which cooperation may find a foothold in a population is if cooperators and defectors are not uniformly distributed in a population—a mechanism termed spatial selection. Neighbors (or friends in a social network) tend to help one another, so in a population with patches of cooperators, these helpful individuals can form clusters that can then grow and thus prevail in competition with defectors. Spatial selection also operates among simpler organisms. Among yeast cells, cooperators make an enzyme used to digest sugar. They do this at a cost to themselves. Defector yeast, meanwhile, mooch off the cooperators' enzymes instead of making their own. Studies conducted by Jeff Gore of the Massachusetts Institute of Technology and, independently, by Andrew Murray of Harvard University have found that among yeast grown in well-mixed populations, the defectors prevailed. In populations with clumps of cooperators and defectors, in contrast, the cooperators won out.

Perhaps one of the most immediately intuitive mechanisms for the evolution of selflessness concerns cooperation among genetically related individuals, or kin selection. In this situation, individuals make sacrifices for their relatives because those relatives share their genes. Thus, although one may be reducing one's own direct reproductive fitness by assisting a relative in need, one is still fostering the spread of those genes the helper shares with recipients. As 20th-century biologist J.B.S. Haldane, who first mentioned the idea of kin selection, put it: "I will jump into the river to save two brothers or eight cousins," referring to the fact that our siblings share 50 percent of our DNA, whereas our first cousins share 12.5 percent. (It turns out that calculating the fitness effects of kin selection is a rather complicated task that has misled many researchers. My colleagues and I are now engaged in an intense debate about the underlying mathematics of kin selection theory.)

The fourth mechanism that fosters the emergence of cooperation is indirect reciprocity, which is quite distinct from the direct variety that Sigmund and I studied initially. In indirect reciprocity, one individual decides to aid another based on the needy individual's reputation. Those who have a reputation for assisting others who fall on hard times might even find themselves on the receiving end of goodwill from strangers when their own luck takes a turn for the worse. Thus, instead of the "I'll scratch your back if you scratch my mine" mentality, the cooperator in this situation might be thinking, "I'll scratch your back, and someone will scratch mine." Among Japanese macaques, for example, low-ranking monkeys that groom high-ranking ones (which have good reputations) may better their own reputations—and hence receive more grooming—simply by being seen with the top brass.

BASICS

## Natural Defection

**A game theory paradox** called the Prisoner's Dilemma illustrates why the existence of cooperation in nature is unexpected. Two people face jail sentences for conspiring to commit a crime. Their sentences depend on whether they elect to cooperate and remain silent or defect and confess to the crime [*see payoff table below*]. Because neither knows what the other will do, the rational choice—the one that always offers the better payoff—is to defect.

| | | INDIVIDUAL 2: COOPERATE (remain silent) | INDIVIDUAL 2: DEFECT (confess) |
|---|---|---|---|
| INDIVIDUAL 1 | COOPERATE (remain silent) | 2 years in jail<br>2 years in jail | 4 years in jail<br>1 year in jail |
| INDIVIDUAL 1 | DEFECT (confess) | 1 year in jail<br>4 years in jail | 3 years in jail<br>3 years in jail |



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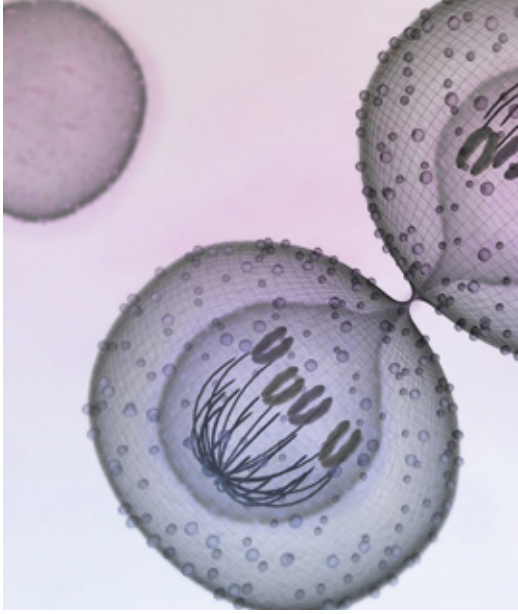
1



3

Last, individuals may perform selfless acts for the greater good, as opposed to abetting a single peer. This fifth means by which cooperation may take root is known as group selection. Recognition of this mechanism dates back to Darwin himself, who observed in his 1871 book *The Descent of Man* that "a tribe including many members who … were always ready to aid one another, and to sacrifice themselves for the common good, would be victorious over most other tribes; and this would be natural selection." Biologists have since argued fiercely over this idea that natural selection can favor cooperation to improve the reproductive potential of the group. Mathematical modeling by researchers, including me, however, has helped show that selection can operate at multiple levels, from individual genes to groups of related individuals to entire species. Thus, the employees of a company compete with one another to move up the corporate ladder, but they also cooperate to ensure that the business succeeds in its competition with other companies.

## ONE FOR ALL

THE FIVE MECHANISMS governing the emergence of cooperation apply to all manner of organisms, from amoebas to zebras (and even, in some cases, to genes and other components of cells). This universality suggests that cooperation has been a driving force in the evolution of life on earth from the beginning. Moreover, there is one group in which the effects of cooperation have proved especially profound: humans. Millions of years of evolution transformed a slow, defenseless ape into the most influential creature on the planet, a species capable of inventing a mind-boggling array of technologies that have allowed our kind to plumb the depths of the ocean, explore outer space and broadcast our achievements to the world in an instant. We have accomplished these monumental feats by working together. Indeed, humans are the most cooperative species—supercooperators, if you will.

Given that the five mechanisms of cooperation occur throughout nature, the question is: What makes humans, in particular, the most helpful of all? As I see it, humans, more than any other creature, offer assistance based on indirect reciprocity, or reputation. Why? Because only humans have full-blown language—and, by extension, names for one another—which allows us to share information about everyone from our immediate family members to complete strangers on the other side of the globe. We are obsessed with who does what to whom and why—we

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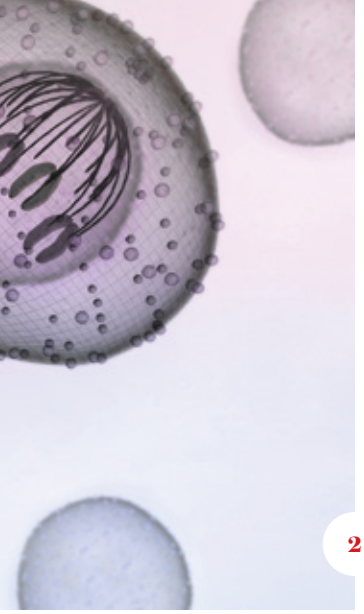

**HELPING OUT:** Leaf-cutter ants work together to carry foliage back to their nest (*1*). Cells regulate their own division to avoid causing cancer (*2*). Lionesses cooperatively rear their young (*3*). Japanese macaques groom each other and thus burnish their reputations in their social group (*4*).

have to be to best position ourselves in the social network around us. Studies have shown that people decide on everything from which charities to sponsor to which corporate start-ups to fund based in part on reputation. My Harvard colleague Rebecca Henderson, an expert on competitive strategy in the business world, notes that Toyota gained a competitive edge over other car manufacturers in the 1980s in part because of its reputation for treating suppliers fairly.

The interplay between language and indirect reciprocity leads to rapid cultural evolution, which is central to our adaptability as a species. As the human population expands and the climate changes, we will need to harness that adaptability and figure out ways to work together to save the planet and its inhabitants. Given our current environmental track record, our odds of meeting that goal do not look great. Here, too, game theory offers insights. Certain cooperative dilemmas that involve more than two players are called public goods games. In this setting, everyone in the group benefits from my cooperation, but all else being equal, I increase my payoff by switching from cooperation to defection. Thus, although I want others to cooperate, my "smart" choice is to defect. The problem is that everyone in the group thinks the same way, and so what begins as cooperation ends in defection.

In the classic public goods scenario known as the Tragedy of the Commons, described in 1968 by the late ecologist Garrett Hardin, a group of livestock farmers who share grazing land allow their animals to overgraze on the communal turf, despite knowing that they are ultimately destroying everyone's resource, including their own. The analogies to real-world concerns about natural resources—from oil to clean drinking water—are obvious. If cooperators tend to defect when it comes to custodianship of communal assets, how can we ever hope to preserve the planet's ecological capital for future generations?

## ALL FOR ONE

THANKFULLY, not all hope is lost. A series of computerized experiments conducted by Manfred Milinski of the Max Planck Institute for Evolutionary Biology in Plön, Germany, and his colleagues have revealed several factors that motivate people to be good stewards of the commons in public goods games. The researchers gave each subject €40 and had them play a game via computer in which the object was to use the money to keep the earth's climate under control. Participants were told that for each round of the game, they had to donate some of their money into a common pool. If at the end of 10 rounds there was €120 or more in the common pool, then the climate was safe and the players would go home with the money they had left over. If they raised less than €120, then the climate would break down and everyone would lose all their money.

Although the players often failed to save the climate, missing the mark by a few euros, the investigators observed differences in their behavior from round to round that hint at what inspires generosity. The researchers found that players were more altruistic when they received authoritative information about climate research, indicating that people need to be convinced that there really is a problem to make sacrifices for the greater good. They also acted more generously when they were allowed to make their contributions publicly rather than anonymously—that is, when their reputation was on the line. Another study by researchers at Newcastle University in England underscored the importance of reputation by finding that people are more generous when they feel they are being watched.

These factors come into play every month when I receive my home's gas bill. The bill compares my household's consumption with both the average household gas consumption in my neighborhood outside Boston and that of the most efficient homes. Seeing how our usage stacks up against our neighbors' motivates my family to use less gas: every winter we try to lower the temperature in the house by one degree Fahrenheit.

Evolutionary simulations indicate that cooperation is intrinsically unstable; periods of cooperative prosperity inevitably give way to defective doom. And yet the altruistic spirit always seems to rebuild itself; our moral compasses somehow realign. Cycles of cooperation and defection are visible in the ups and downs of human history, the oscillations of political and financial systems. Where we humans are in this cycle right now is uncertain, but clearly we could be doing a better job of working together to solve the world's most pressing problems. Game theory suggests a way. Policy makers should take note of indirect reciprocity and the importance of information and reputation in keeping defectors in check. And they should exploit the capacity of these factors to make better cooperators of us all in the mother of all public goods games: the seven-billion-person mission to conserve the rapidly dwindling resources of planet Earth. SA

### MORE TO EXPLORE


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View a slide show of cooperative species at ScientificAmerican.com/jul2012/cooperation

GETTY IMAGES (*cells*); OSCAR TARNEBERG *Getty Images (monkeys)*



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GENETICS

# How We Are Evolving

Analyses of our DNA suggest that recent human evolution has occurred more slowly than biologists would have expected

BY JONATHAN K. PRITCHARD


IN BRIEF

**As early *Homo sapiens*** spread out from Africa starting around 60,000 years ago, they encountered environmental challenges that they could not overcome with prehistoric technology.

**Many scientists** thus expected that surveys of our genomes would reveal considerable evidence of novel genetic mutations that have recently spread quickly throughout different populations by natural selection—that is, because those who carry the mutations have greater numbers of healthy babies than those who do not.

**But it turns out** that although the genome contains some examples of very strong, rapid natural selection, most of the detectable natural selection appears to have occurred at a far slower pace than researchers had envisioned.


*Illustrations by Owen Gildersleeve*



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THOUSANDS OF YEARS AGO HUMANS MOVED FOR THE FIRST TIME INTO THE TIBETAN plateau, a vast expanse of steppelands that towers some 14,000 feet above sea level. Although these trailblazers would have had the benefit of entering a new ecosystem free of competition with other people, the low oxygen levels at that altitude would have placed severe stresses on the body, resulting in chronic altitude sickness and high infant mortality. Two years ago a flurry of genetic studies identified a gene variant that is common in Tibetans but rare in other populations. This variant, which adjusts red blood cell production in Tibetans, helps to explain how this group adapted to those harsh conditions. The discovery, which made headlines around the world, provided a dramatic example of how humans have undergone rapid biological adaptation to new environmental circumstances in the recent past. One study estimated that the beneficial variant spread to high frequency within the past 3,000 years—a mere instant in evolutionary terms.

The Tibet findings seemed to bolster the notion that our species has undergone considerable biological adaptation of this sort since it first left Africa perhaps 60,000 years ago (estimates range from 50,000 to 100,000 years ago). The transition to high altitude is just one of many environmental challenges *Homo sapiens* encountered as it migrated from the hot grasslands and shrublands of East Africa to frigid tundras, steamy rain forests and sun-baked deserts—practically every terrestrial ecosystem and climate zone on the planet. To be sure, much of human adaptation was technological—to combat the cold, for instance, we made clothing. But prehistoric technology alone could not have been enough to overcome thin mountain air, the ravages of infectious disease and other environmental obstacles. In these circumstances, adaptation would have to occur by genetic evolution rather than through technological solutions. It was reasonable to expect, then, that surveys of our genomes would reveal considerable evidence of novel genetic mutations that have spread recently throughout different populations by natural selection—that is, because those who carry the mutations have more healthy babies who survive to reproduce than those who do not.

**It is possible that human genomes have undergone more adaptive change recently than scientists can yet identify by examining the genome in the usual way.**

Eight years ago my colleagues and I set out to look for the imprints of these profound environmental challenges on the human genome. We wanted to figure out how humans have evolved since our predecessors set out on their relatively recent global journey. To what extent do populations in disparate parts of the world differ genetically because natural selection recently adapted them to different environmental pressures, as in the case of the Tibetans? What proportion of these genetic differences stems instead from other influences? Thanks to advances in technologies for studying genetic variation, we were able to begin to address these questions.

The work is still under way, but the preliminary findings have surprised us. It turns out that the genome actually contains few examples of very strong, rapid natural selection. Instead most of the natural selection visible in the genome appears to have occurred over tens of thousands of years. What seems to have happened in many cases is that a beneficial mutation spread through a population long ago in response to a local environmental pressure and then was carried into faraway locales as the population expanded into new territories. For example, some gene variants involved in determining light skin color, an adaptation to reduced sunlight, are distributed according to ancient migration routes, rather than just latitude. That these ancient selection signals have persisted over millennia without new environmental pressures overwriting them indicates that natural selection often operates at a far more leisurely pace than scientists had envisioned. The rapid evolution of a major gene in the Tibetans, it appears, is not typical.

As an evolutionary biologist, I am often asked whether humans are still evolving today. We certainly are. But the answer to the question of how we are changing is far more complicated. Our data suggest that the classic natural selection scenario, in which a single beneficial mutation spreads like wildfire through a population, has actually occurred relatively rarely in humans in the past 60,000 years. Rather this mechanism of evolutionary change usually seems to require consistent environmental pressures over tens of thousands of years—an uncommon situation once our ancestors started globe-trotting and the pace of technological innovation began accelerating.

Already these findings are helping to refine our understanding not only of recent human evolution but also of what our collective future might hold. For a number of the challenges currently facing our species—global climate change and many infectious diseases, for example—natural selection probably occurs too slowly to help us much. Instead we are going to have to rely on culture and technology.

## FINDING THE FOOTPRINTS

JUST A DECADE AGO it was extremely difficult for scientists to trace our species' genetic responses to our environment; the needed tools just did not exist. All that changed with the completion of the human genome sequence and the subsequent cataloguing of genetic variation. To understand exactly what we did, it helps to know a bit about how DNA is structured and how small changes can affect its function. The human genome sequence consists of about



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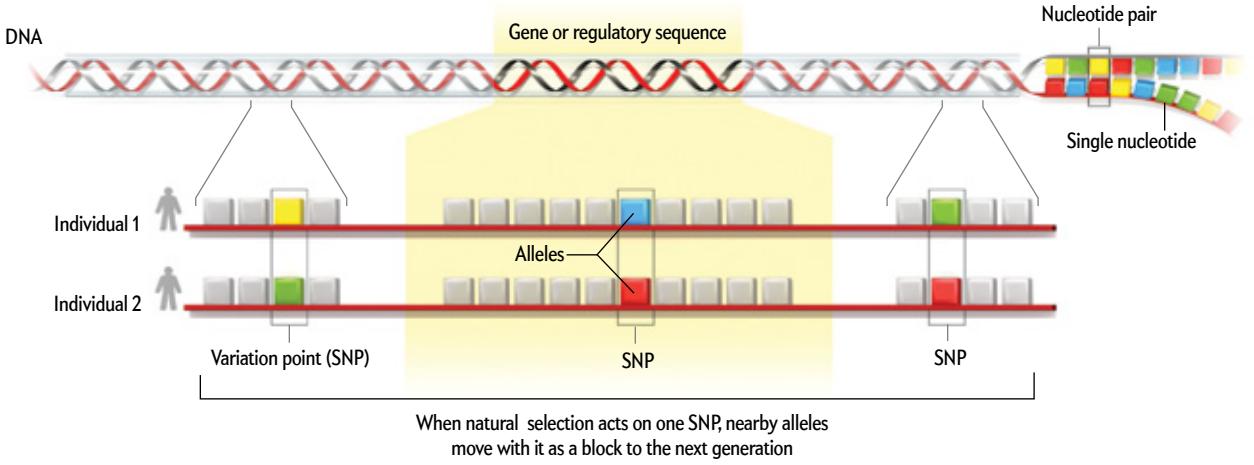
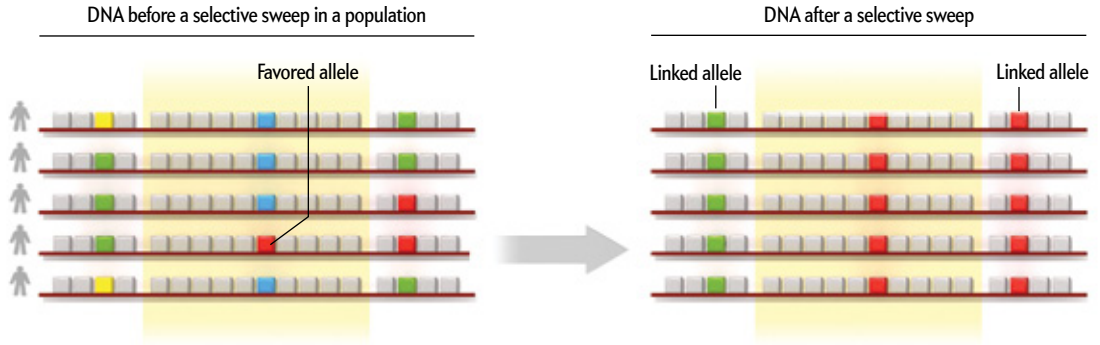
# Selection Signal

**Scientists can infer that natural selection** has acted on a region of DNA if they observe a lack of variability in that region. The genomes of any two people differ at only approximately one out of every 1,000 pairs of DNA nucleotides, or "letters." These points of difference are known as single-nucleotide polymorphisms (SNPs), and the alternative versions of nucleotides at each SNP are called alleles. When a particular allele ends up improving reproductive success, it ultimately spreads through a population, or is "selected." At the same time, nearby alleles travel along with the favored one and thus become more common in the population as well. The resulting reduction of SNP variation in this part of the genome in a population is termed a selective sweep.




three billion pairs of DNA nucleotides, or "letters," that serve as an instruction manual for how to assemble a human [*see box above*]. The manual is now known to contain a parts list of about 20,000 genes—strings of DNA letters that spell out the information required to build proteins. (Proteins, which include enzymes, do much of the work in cells.) About 2 percent of the human genome encodes proteins, and a somewhat larger fraction is involved in gene regulation. Most of the rest of the genome has no known role.

Overall the genomes of any two people are extremely similar, differing in only about one out of every 1,000 nucleotide pairs. Sites where one nucleotide pair substitutes for another are referred to as single-nucleotide polymorphisms, or SNPs (pronounced "snips"), and the alternative versions of the DNA at each SNP are called alleles. Because most of the genome does not encode proteins or regulate genes, most SNPs probably have no measurable effect on the individual. But if a SNP occurs in a region of the genome that does have a coding or regulating function, it may affect the structure or function of a protein or where and how much of the protein is made. In this way, SNPs can conceivably modify almost any trait, be it height, eye color, ability to digest milk, or susceptibility to diseases such as diabetes, schizophrenia, malaria and HIV.

When natural selection strongly favors a particular allele, it becomes more common in the population with each generation, while the disfavored allele becomes less common. Eventually, if the environment remains stable, the beneficial allele will spread until everyone in the population carries it, at which point it has become fixed in that group. This process typically takes many generations. If a person with two copies of the beneficial allele pro-

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*Illustration by Emily Cooper*



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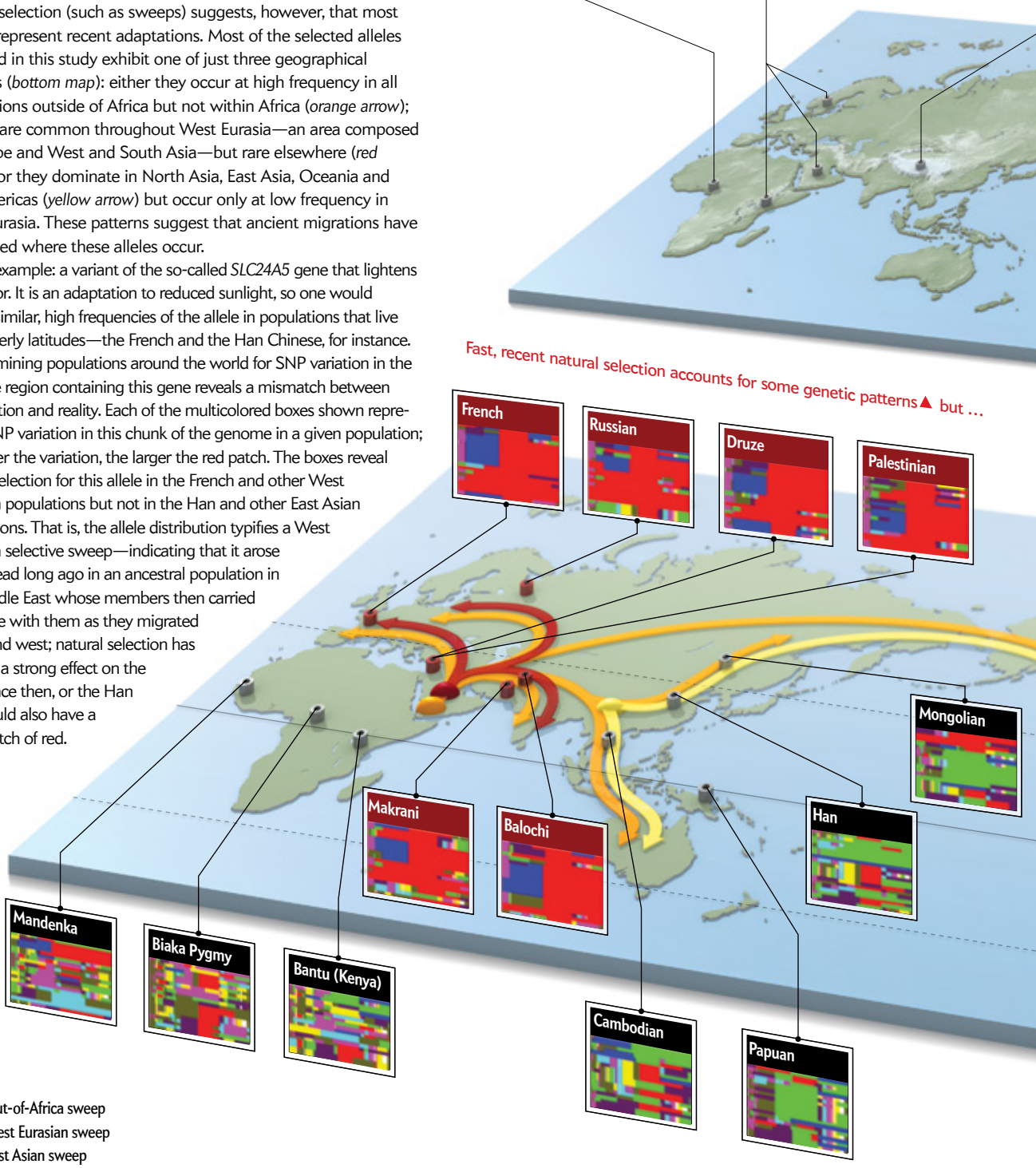
# Surprising Findings from Population Studies

**Researchers have identified** a handful of favorable alleles that spread to high frequency as a result of strong natural selection acting quickly to adapt people to local environmental pressures (*right*). A new analysis of hundreds of other apparent signals of natural selection (such as sweeps) suggests, however, that most do not represent recent adaptations. Most of the selected alleles detected in this study exhibit one of just three geographical patterns (*bottom map*): either they occur at high frequency in all populations outside of Africa but not within Africa (*orange arrow*); or they are common throughout West Eurasia—an area composed of Europe and West and South Asia—but rare elsewhere (*red arrow*); or they dominate in North Asia, East Asia, Oceania and the Americas (*yellow arrow*) but occur only at low frequency in West Eurasia. These patterns suggest that ancient migrations have influenced where these alleles occur.

An example: a variant of the so-called *SLC24A5* gene that lightens skin color. It is an adaptation to reduced sunlight, so one would expect similar, high frequencies of the allele in populations that live at northerly latitudes—the French and the Han Chinese, for instance. But examining populations around the world for SNP variation in the genome region containing this gene reveals a mismatch between expectation and reality. Each of the multicolored boxes shown represents SNP variation in this chunk of the genome in a given population; the lower the variation, the larger the red patch. The boxes reveal strong selection for this allele in the French and other West Eurasian populations but not in the Han and other East Asian populations. That is, the allele distribution typifies a West Eurasian selective sweep—indicating that it arose and spread long ago in an ancestral population in the Middle East whose members then carried the allele with them as they migrated north and west; natural selection has not had a strong effect on the gene since then, or the Han box would also have a large patch of red.

A gene known as *LARGE* that participates in the body's response to infection with the Lassa fever virus has undergone strong, recent natural selection in a population in Nigeria, where the pathogen is endemic.

The gene for the lactase enzyme that digests the sugar in milk has undergone rapid evolution among dairy-farming populations in Europe, the Middle East and East Africa over the past 5,000 to 10,000 years.




*Maps by Emily Cooper*



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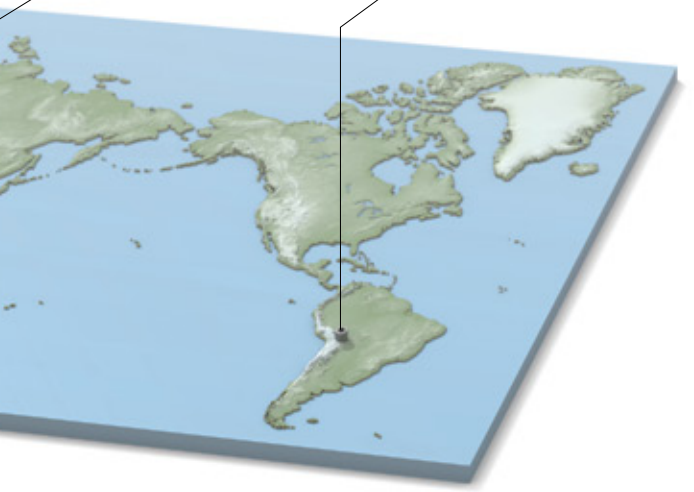
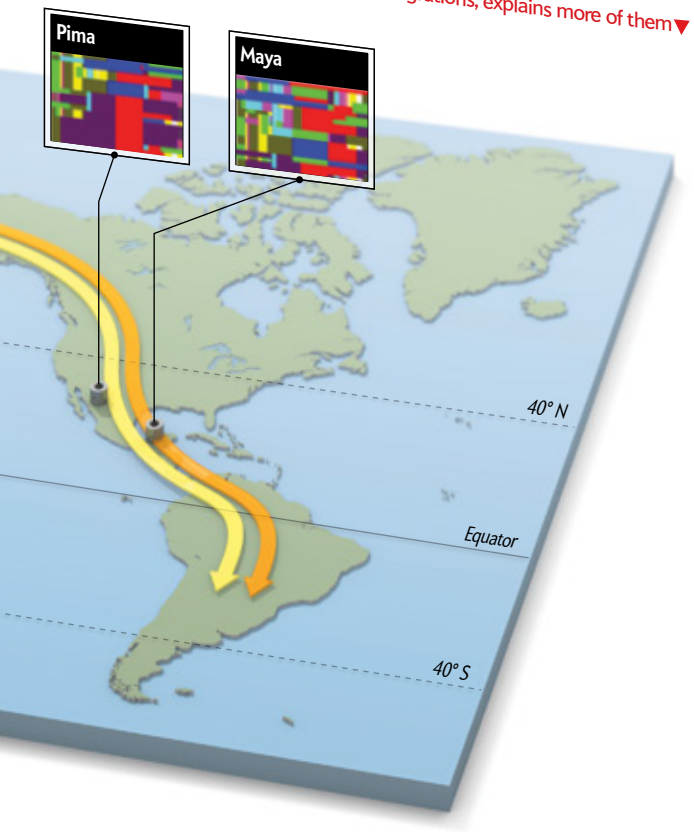
A rare variant of a gene called hypoxia-inducible factor 2-alpha has spread to high frequency in Tibetans over the past few thousand years, helping to mitigate the ill effects of living at altitudes up to 14,000 feet above sea level by adjusting red blood cell production.

In women who inhabit the Bolivian Altiplano, some 12,000 feet above sea level, the uterine artery undergoes accelerated growth during pregnancy compared with the growth seen in women from low-lying regions—an adaptation that has evolved within the past 10,000 years.



… slow selection, coupled with ancient migrations, explains more of them ▼




SOURCE: "THE ROLE OF GEOGRAPHY IN HUMAN ADAPTATION," BY GRAHAM COOP ET AL., IN *PLoS GENETICS*, VOL. 5, NO. 6; JUNE 2009 *(haplotype patterns)*

duces 10 percent more children and someone with one copy produces 5 percent more, on average, than someone without the beneficial allele, then it will take that allele about 200 generations, or roughly 5,000 years, to increase in frequency from 1 percent of the population to 99 percent of it. In theory, a helpful allele could become fixed in as little as a few hundred years if it conferred an extraordinarily large advantage. Conversely, a less advantageous allele could take many thousands of years to spread.

It would be great if in our efforts to understand recent human evolution, we could obtain DNA samples from ancient remains and actually track the changes of favored alleles over time. But DNA usually degrades quickly in ancient samples, thereby hindering this approach. Thus, my research group and a number of others around the world have developed methods of examining genetic variation in modern-day humans for signs of natural selection that has happened in the past.

One such tactic is to comb DNA data from many different people for stretches that show few differences in SNP alleles within a population. When a new beneficial mutation propagates rapidly through a group because of natural selection, it takes a surrounding chunk of the chromosome with it in a process called genetic hitchhiking. As the frequency of the beneficial allele increases in the group over time, so, too, do the frequencies of nearby "neutral" and nearly neutral alleles that do not affect protein structure or amount appreciably but ride along with the selected allele. The resulting reduction or elimination of SNP variation in the region of the genome containing a beneficial allele is termed a selective sweep. The spread of selected alleles by natural selection can also leave other distinctive patterns in the SNP data: if an existing allele suddenly proves particularly helpful when a population finds itself in new circumstances, that allele can reach high frequency (while remaining rare in other populations) without necessarily generating a hitchhiking signal.

Over the past few years multiple studies, including one my colleagues and I published in 2006, have identified several hundred genome signals of apparent natural selection that occurred within the past 60,000 years or so—that is, since *H. sapiens* left Africa. In a few of these cases, scientists have a pretty good grasp on the selective pressures and the adaptive benefit of the favored allele. For example, among dairy-farming populations in Europe, the Middle East and East Africa, the region of the genome that houses the gene for the lactase enzyme that digests lactose (the sugar in milk) shows clear signs of having been the target of strong selection. In most populations, babies are born with the ability to digest lactose, but the lactase gene turns off after weaning, leaving people unable to digest lactose as adults. Writing in the *American Journal of Human Genetics* in 2004, a team at the Massachusetts Institute of Technology estimated that variants of the lactase gene that remain active into adulthood achieved high frequency in European dairy-farming groups in just 5,000 to 10,000 years. In 2006 a group led by Sarah Tishkoff, now at the University of Pennsylvania, reported in *Nature Genetics* that they had found rapid evolution of the lactase gene in East African dairy-farming populations. These changes were surely an adaptive response to a new subsistence practice.

Researchers have also found pronounced signals of selection in at least half a dozen genes involved in determining skin, hair and eye color in non-Africans. Here, too, the selective pressure and adaptive benefit are clear. As humans moved out of their



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tropical homeland, they received reduced ultraviolet radiation from the sun. The body requires UV radiation to synthesize vitamin D, an essential nutrient. In the tropics, UV radiation is strong enough to penetrate dark skin in amounts needed for vitamin D synthesis. Not so in the higher latitudes. The need to absorb adequate amounts of vitamin D almost certainly drove the evolution of lighter skin color in these locales, and changes in these genes that bear signals of strong selection enabled that adaptive shift.

Selection signals also show up in a variety of genes that confer resistance to infectious diseases. For instance, Pardis Sabeti of Harvard University and her colleagues have found a mutation in the so-called *LARGE* gene that has recently spread to high frequency in the Yoruba people of Nigeria and is probably a response to the relatively recent emergence of Lassa fever in this region.

## MIXED SIGNALS

THOSE EXAMPLES and a small number of other cases provide strong evidence of natural selection acting quickly to promote helpful alleles. For most of the rest of the hundreds of candidate signals, however, we do not yet know which environmental factors favored the spread of the selected allele, nor do we know what effect the allele exerts on the people who harbor it. Until recently, we and others interpreted these candidate signals to mean that there have been at least a few hundred very rapid selective sweeps within the past 15,000 years in several human populations that have been studied. But in newer work my colleagues and I have found evidence suggesting that instead most of these signals are not actually the result of very recent, rapid adaptation to local conditions at all.

Working with collaborators at Stanford University, we studied a massive SNP data set generated from DNA samples obtained from about 1,000 individuals from around the world. When we looked at the geographical distributions of selected alleles, we found that the most pronounced signals tend to fall into one of just three geographical patterns. First there are the so-called out-of-Africa sweeps, in which the favored allele and its hitchhikers exist at high frequency in all non-African populations [*see box on preceding two pages*]. This pattern suggests that the adaptive allele appeared and began to spread very shortly after humans left Africa but while they were still restricted to the Middle East—thus perhaps around 60,000 years ago—and was subsequently carried around the globe as humans migrated north and east. Then there are two other, more restricted, geographical patterns: the West Eurasian sweeps, in which a favored allele occurs at high frequency in all of the populations of Europe, the Middle East, and Central and South Asia, but not elsewhere; and the East Asian sweeps, in which the favored allele is most common in East Asians, as well as usually Native Americans, Melanesians and Papuans. These two patterns probably represent sweeps that got under way shortly after the West Eurasians and East Asians split off and went their separate ways. (It is not known precisely when this occurred, but probably around 20,000 to 30,000 years ago.)

These sweep patterns reveal something very interesting: ancient population movements have heavily influenced the distributions of favored alleles across the globe, and natural selection has done little to fine-tune those distributions to match modern environmental pressures. For example, one of the most important players in the adaptation to lighter skin color is a variant of the so-called *SLC24A5* gene. Because it is an adaptation to reduced sunlight, one might expect its frequency in the population to increase with latitude and its distribution to be similar in people from North Asia and northern Europe. Instead we see a West Eurasian sweep: the gene variant and the hitchhiking DNA that travels with it are common from Pakistan to France but essentially absent in East Asia—even in the northern latitudes. This distribution indicates that the beneficial variant arose in the ancestral population of the West Eurasians—after they diverged from the ancestors of the East Asians—who carried it throughout that region. Thus, natural selection drove the beneficial *SLC24A5* allele to high frequency early on, but ancient population history helped to determine which populations today have it and which do not. (Other genes account for light skin in East Asians.)

A closer look at the selection signals in these and other data reveals another curious pattern. Most of the alleles with the most extreme frequency differences between populations—those that occur in nearly all Asians but no Africans, for example—do not exhibit the strong hitchhiking signals one would expect to



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see if natural selection swiftly drove these new alleles to high frequency. Instead these alleles seem to have propagated gradually during the roughly 60,000 years since our species set out from Africa. In light of these observations, my collaborators and I now believe that textbook selective sweeps—in which natural selection drives an advantageous new mutation rapidly to fixation—have actually occurred fairly rarely in the time since the *H. sapiens* diaspora began. We suspect that natural selection usually acts relatively weakly on individual alleles, thus promoting them very slowly. As a result, most alleles experiencing selection pressure may attain high frequency only when the pressure persists for tens of thousands of years.

**The genome actually contains few examples of very strong, rapid natural selection. Instead most of the visible natural selection appears to have occurred over tens of thousands of years.**

### ONE TRAIT, MANY GENES

OUR CONCLUSIONS may seem paradoxical: if it usually has taken 50,000, not 5,000, years for a helpful allele to spread through a population, how would humans ever manage to adapt quickly to new conditions? Although the best understood adaptations arise from changes in a single gene, it may be that most adaptations do not arise that way but rather stem from genetic variants having mild effects on hundreds or thousands of relevant genes from across the genome—which is to say they are polygenic. A paper published in 2010, for example, identified more than 180 different genes that influence human height, and certainly many more remain to be found. For each of these, one allele increases average height by only about one to five millimeters compared with another allele.

When natural selection targets human height—as has occurred in the pygmy populations that live in rain forest habitats in Africa, Southeast Asia and South America, where small body size may be an adaptation to the limited nutrition available in these environments—it may operate in large part by tweaking the allele frequencies of hundreds of different genes. If the "short" version of every height gene became just 10 percent more common, then most people in the population would have a larger number of "short" alleles, and the population would be shorter overall. Even if the overall trait were under strong selection, the strength of selection on each individual height gene would still be weak. Because the selection acting on any one gene is weak, polygenic adaptations would not show up in genome studies as a classic signal of selection. Thus, it is possible that human genomes have undergone more adaptive change recently than scientists can yet identify by examining the genome in the usual way.

### STILL EVOLVING?

AS TO WHETHER HUMANS are still evolving, it is difficult to catch natural selection in the act of shaping present-day populations. It is, however, easy to imagine traits that might be affected. Infectious diseases such as malaria and HIV continue to exert potent selection forces in the developing world. The handful of known gene variants that provide some measure of protection against these scourges are probably under strong selective pressure because people who carry them are more likely to survive and live to have many more children than those who do not. A variant that shields carriers from the *vivax* form of malaria has become ubiquitous in many populations in sub-Saharan Africa. The variants that protect against HIV, meanwhile, could spread throughout sub-Saharan Africa in hundreds of years if the virus were to persist and continue to be thwarted by that resistance gene. But given that HIV is evolving faster than humans are, we are more likely to overcome that problem with technology (in the form of a vaccine, for example) than with natural selection.

In the developed world relatively few people die between birth and adulthood, so some of the strongest selection forces are probably those acting on genes that affect the number of children each person produces. In principle, any aspect of fertility or reproductive behavior that genetic variation affects could be the target of natural selection. Writing in the *Proceedings of the National Academy of Sciences USA* in 2009, Stephen C. Stearns of Yale University and his colleagues reported on the results of a study that identified six different traits in women that are associated with higher lifetime numbers of children and that all show intermediate to high heritability. Women with larger numbers of children, the team found, tend to be slightly shorter and stouter than average and to have a later age at menopause. Hence, if the environment stays constant, these traits will presumably become more common over time because of natural selection: the authors estimate that the average age at menopause will increase by about one year over the next 10 generations, or 200 years. (More speculatively, it is plausible that genetic variation influencing sexual behavior—or use of contraceptives—would be subject to strong selection, although just how strongly genes affect complex behaviors such as these remains unclear.)

Still, the rate of change of most traits is glacially slow compared with the rate at which we change our culture and technology and, of course, our global environment. And major adaptive shifts require stable conditions across millennia. Thus, 5,000 years from now the human milieu will no doubt be very different. But in the absence of large-scale genomic engineering, people themselves will probably be largely the same. SA

### MORE TO EXPLORE


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# What May Become of *Homo sapiens*

Conditions of modern life could be driving changes in the makeup of our genes. Our bodies and our brains may not be the same as those of our descendants

BY PETER WARD

**IN BRIEF**

**People commonly assume** that our species has evolved very little since prehistoric times. Yet new studies using genetic information from populations around the globe suggest that the pace of human evolution increased with the advent of agriculture and cities.

**If we are still evolving,** what might our species look like in a millennium should we survive whatever environmental and social surprises are in store for us? Speculation ranges from the hopeful to the dystopian.

WHEN YOU ASK FOR OPINIONS ABOUT WHAT FUTURE HUMANS might look like, you typically get one of two answers. Some people trot out the old science-fiction vision of a big-brained human with a high forehead and higher intellect. Others say humans are no longer evolving physically—that technology has put an end to the brutal logic of natural selection and that evolution is now purely cultural.

The big-brain vision has no real scientific basis. The fossil record of human skull sizes over the past several thousand generations shows that our days of rapid increase in brain size are long over. Accordingly, most scientists a few years ago would have taken the view that human physical evolution has essentially ceased. But DNA techniques, which probe genomes both present and past, have unleashed a revolution in studying evolution; they tell a different story. Not only has *Homo sapiens* been doing some major genetic reshuffling since our species formed, but the rate of human evolution may, if anything, have increased. In common with other organisms, we underwent the most dramatic changes to our body shape when our species first appeared, but we continue to show genetically induced changes to our physiology and perhaps to our behavior as well. Until fairly recently in our history, human races in various parts of the world were becoming more rather than less distinct. Even today the conditions of modern life could be driving changes to genes for certain behavioral traits.

If giant brains are not in store for us, then what is? Will we become larger or smaller, stronger or weaker, smarter or dumber? How will the emergence of new diseases and the rise in global temperature shape us? Will a new human species arise one day? Or does the future evolution of humanity lie not within our genes but within our technology, as we augment our brains and bodies with silicon and steel? Are we but the builders of the next dominant intelligence on the earth—the machines?

KEVIN SUMMERS Getty Images (flower); PAUL TAYLOR Getty Images (hand); RON LEVINE Getty Images (girl); PHOTODISC Getty Images (brain); ISTOCKPHOTO (skull and egg)

*Photoillustrations by Nessim Higsom*



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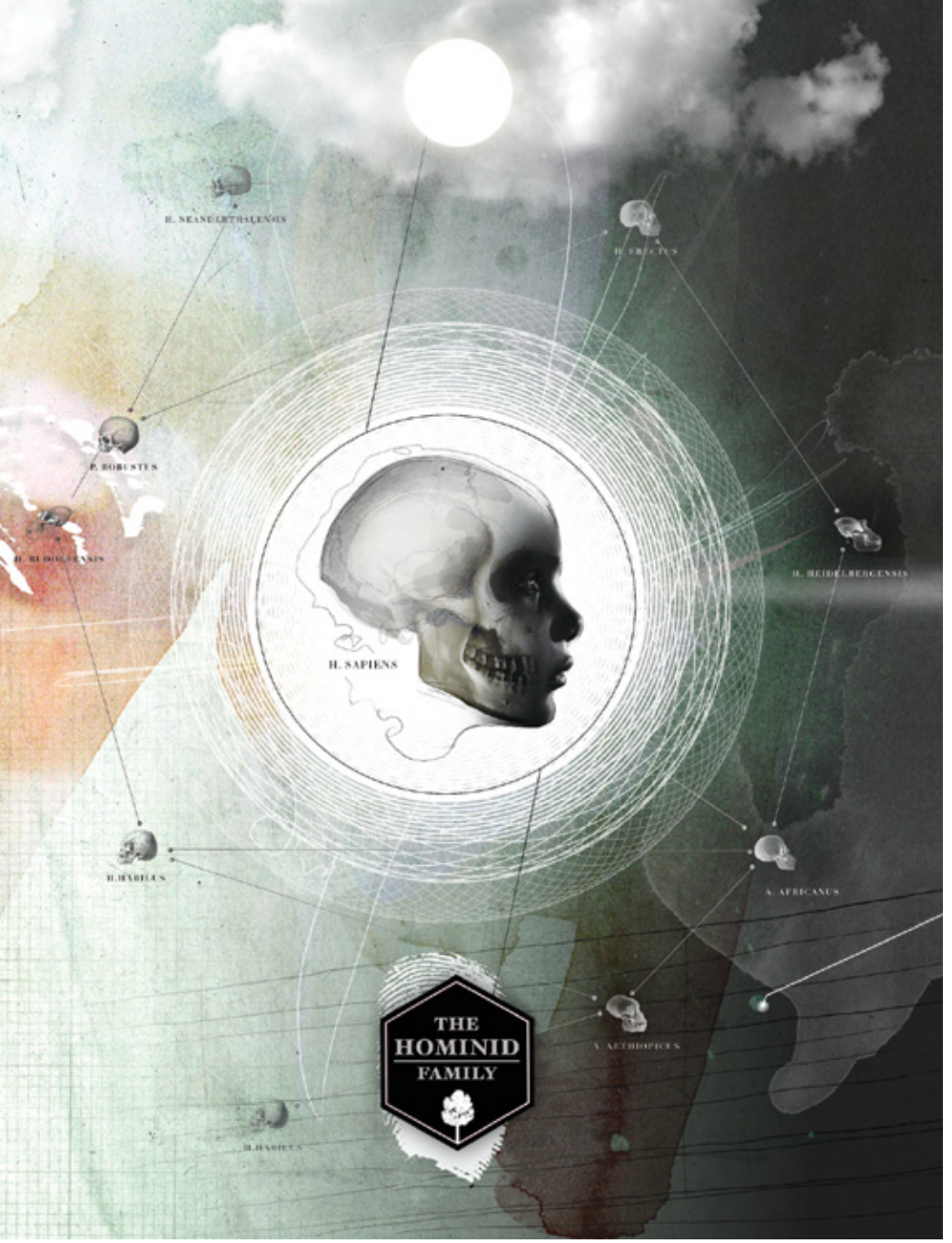


**Over the past 10,000 years humans have evolved as much as 100 times faster than at any other time.**

### THE FAR AND RECENT PAST

TRACKING HUMAN EVOLUTION used to be the province solely of paleontologists, those of us who study fossil bones from the ancient past. The human family, called the Hominidae, goes back at least seven million years to the appearance of a small protohuman called *Sahelanthropus tchadensis*. Since then, our family has had a still disputed, but rather diverse, number of new species in it—as many as nine that we know of and others surely still hidden in the notoriously poor hominid fossil record. Because early human skeletons rarely made it into sedimentary rocks before they were scavenged, this estimate changes from year to year as new discoveries and new interpretations of past bones make their way into print.

Each new species evolved when a small group of hominids somehow became separated from the larger population for many generations and then found itself in novel environmental conditions favoring a different set of adaptations. Cut off from kin, the small population went its own genetic route and eventually its members could no longer successfully reproduce with the parent population.

The fossil record tells us that the oldest member of our own species lived 195,000 years ago in what is now Ethiopia. From there *Homo sapiens* spread out across the globe. By 10,000 years ago modern humans had successfully colonized each of the continents save Antarctica, and adaptations to these many locales (among other evolutionary forces) led to what we loosely call races. Groups living in different places evidently retained just enough connections with one another to avoid evolving into separate species. With the globe fairly well covered, one might expect that the time for evolving was pretty much finished.

But that turns out not to be the case. In a study published in 2007 Henry C. Harpending of the University of Utah, John Hawks of the University of Wisconsin–Madison and their colleagues analyzed data from the international haplotype map of the human genome [see "Traces of a Distant Past," by Gary Stix, on page 60]. They focused on genetic markers in 270 people from four groups: Han Chinese, Japanese, Yoruba and northern Europeans. They found that at least 7 percent of human genes underwent evolution as recently as 5,000 years ago. Much of the change involved adaptations to particular environments, both natural and human-shaped. For example, few people in China and Africa can digest fresh milk into adulthood, whereas almost everyone in Sweden and Denmark can. This ability presumably arose as an adaptation to dairy farming.

Another study by Pardis C. Sabeti of Harvard University and her colleagues used huge data sets of genetic variation to look for signs of natural selection across the human genome. More than 300 regions on the genome showed evidence of recent changes that improved people's chance of surviving and reproducing. Examples included resistance to one of Africa's great scourges, the virus causing Lassa fever; partial resistance to

ISTOCKPHOTO (*skull and boy's head*)



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other diseases, such as malaria, among some African populations; changes in skin pigmentation and development of hair follicles among Asians; and the evolution of lighter skin and blue eyes in northern Europe.

Harpending and Hawks's team estimated that over the past 10,000 years humans have evolved as much as 100 times faster than at any other time since the split of the earliest hominid from the ancestors of modern chimpanzees. The team attributed the quickening pace to the variety of environments humans moved into and the changes in living conditions brought about by agriculture and cities. It was not farming per se or the changes in the landscape that conversion of wild habitat to tamed fields brought about but the often lethal combination of poor sanitation, novel diet and emerging diseases (from other humans as well as domesticated animals). Although some researchers have expressed reservations about these estimates, the basic point seems clear: humans are first-class evolvers.

**PETER WARD** has been active in paleontology, biology and astrobiology for more than 30 years. He led the University of Washington node of the NASA Astrobiology Institute, a team of more than 40 scientists and students, from 2001 to 2006. Ward is especially known as an expert on mass extinctions and the role of extraterrestrial impacts on the earth. He is working more and more in conservation biology, including studies of how nautiluses—marine "living fossils" that have changed little over millions of years—attempt to evade capture by ever more clever humans using ever better technology.

## UNNATURAL SELECTION

DURING THE PAST CENTURY, our species' circumstances have again changed. The geographical isolation of different groups has been broached by the ease of transportation and the dismantling of social barriers that once kept racial groups apart. Never before has the human gene pool had such widespread mixing of what were heretofore entirely separated local populations of our species. In fact, the mobility of humanity might be bringing about the homogenization of our species. At the same time, natural selection in our species is being thwarted by our technology and our medicines. In most parts of the globe, babies no longer die in large numbers. People with genetic damage that was once fatal now live and have children. Natural predators no longer affect the rules of survival.

Steve Jones of University College London has argued that human evolution has essentially ceased. At a Royal Society of Edinburgh debate in 2002 entitled "Is Evolution Over?" he said: "Things have simply stopped getting better, or worse, for our species. If you want to know what Utopia is like, just look around—this is it." Jones suggested that, at least in the developed world, almost everyone has the opportunity to reach reproductive age, and the poor and rich have an equal chance of having children. Inherited disease resistance—say, to HIV—may still confer a survival advantage, but culture, rather than genetic inheritance, is now the deciding factor in whether people live or die. In short, evolution may now be memetic—involving ideas—rather than genetic.

Another point of view is that genetic evolution continues to occur even today, but in reverse. Certain characteristics of modern life may drive evolutionary change that does not make us fitter for survival—or that even makes us less fit. Innumerable college students have noticed one potential way that such "inadaptive" evolution could happen: they put off reproduction while many of their high school classmates who did not make the grade started having babies right away. If less intelligent parents have more kids, then intelligence is a Darwinian liability in today's world, and average intelligence might evolve downward.

Such arguments have a long and contentious history. One of the many counterarguments is that human intelligence is made up of many different abilities encoded by a large number of genes. It thus has a low degree of heritability, the rate at which one generation passes the trait to the next. Natural selection acts only on heritable traits. Researchers actively debate just how heritable intelligence is, but they have found no sign that average intelligence is in fact decreasing.

Even if intelligence is not at risk, some scientists speculate that other, more heritable traits could be accumulating in the human species and that these traits are anything but good for us. For instance, behavior disorders such as Tourette's syndrome and attention-deficit hyperactivity disorder (ADHD) may, unlike intelligence, be encoded by but a few genes, in which case their heritability could be very high. If these disorders increase one's chance of having children, they could become ever more prevalent with each generation. David Comings, a specialist in these two diseases, has argued in scientific papers and a 1996 book that these conditions are more common than they used to be and that evolution might be one reason: women with these syndromes are less likely to attend college and thus tend to have more children than those who do not. But other researchers have brought forward serious concerns about Comings's methodology. It is not clear whether the incidence of Tourette's and ADHD is, in fact, increasing at all. Research into these areas is also made more difficult because of the perceived social stigma that many of these afflictions attach to their carriers.

Although these particular examples do not pass scientific muster, the basic line of reasoning is plausible. We tend to think of evolution as something involving structural modification, yet it can and does affect things invisible from the outside—behavior. Many people carry the genes making them susceptible to

SPECIATION

## Beyond *Homo sapiens*

**Our lineage** has produced new species in the past. What about the future? Speciation requires an isolating mechanism of some kind. The most common is geographical isolation, where a small population gets cut off from the larger gene pool. The very size and interconnectedness of humanity make this possibility low under present conditions, but here are some ways to bring it about:

- Setting up human colonies on distant worlds.
- Losing or voluntarily discarding the technology that allows the global interchange of our genes.
- Breaking into isolated groups after an apocalypse such as a large asteroid hitting the earth.
- Engaging in genetic engineering.



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alcoholism, drug addiction and other problems. Most do not succumb, because genes are not destiny; their effect depends on our environment. But others do succumb, and their problems may affect whether they survive and how many children they have. These changes in fertility are enough for natural selection to act on. Much of humanity's future evolution may involve new sets of behaviors that spread in response to changing social and environmental conditions. Of course, humans differ from other species in that we do not have to accept this Darwinian logic passively.

### DIRECTED EVOLUTION

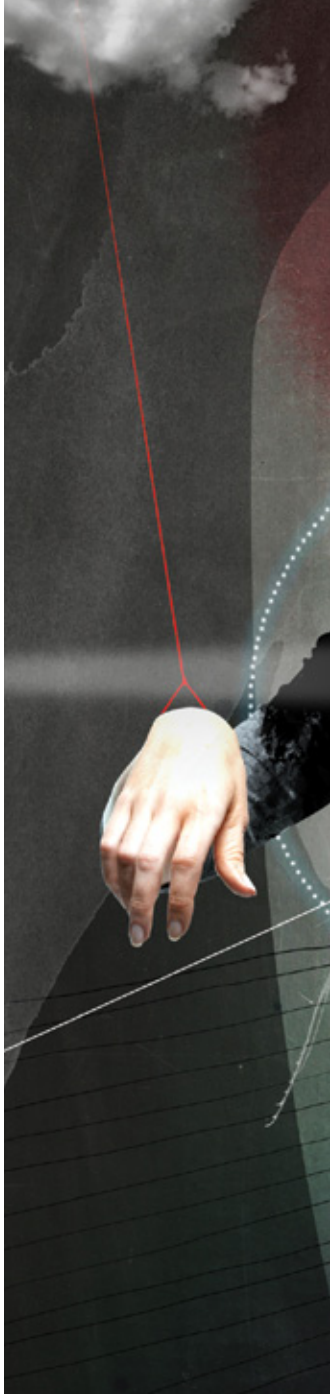
WE HAVE DIRECTED the evolution of so many animal and plant species. Why not direct our own? Why wait for natural selection to do the job when we can do it faster and in ways beneficial to ourselves? In the area of human behavior, for example, geneticists are tracking down the genetic components not just of problems and disorders but also of overall disposition and various aspects of sexuality and competitiveness, many of which may be at least partially heritable. Over time, elaborate screening for genetic makeup may become commonplace, and people will be offered drugs based on the results.

The next step will be to actually change people's genes. That could conceivably be done in two ways: by changing genes in the relevant organ only (gene therapy) or by altering the entire genome of an individual (what is known as germ-line therapy). Researchers are still struggling with the limited goal of gene therapy to cure disease. But if they can ever pull off germ-line therapy, it will help not only the individual in question but also his or her children. The major obstacle to genetic engineering in humans will be the sheer complexity of the genome. Genes usually perform more than one function; conversely, functions are usually encoded by more than one gene. Because of this property, known as pleiotropy, tinkering with one gene can have unintended consequences.

Why try at all, then? The pressure to change genes will probably come from parents wanting to guarantee their child is a boy or a girl; to endow their children with beauty, intelligence, musical talent or a sweet nature; or to try to ensure that they are not helplessly disposed to become mean-spirited, depressed, hyperactive or even criminal. The motives are there, and they are very strong. Just as the push by parents to genetically enhance their children could be socially irresistible, so, too, would be an assault on human aging. Many recent studies suggest that aging is not so much a simple wearing down of body parts as it is a programmed decay, much of it genetically controlled. If so, the next century of genetic research could unlock numerous genes controlling many aspects of aging. Those genes could be manipulated.

Assuming that it does become practical to change our genes, how will that affect the future evolution of humanity? Probably a great deal. Suppose parents alter their unborn children to enhance their intelligence, looks and longevity. If the kids are as smart as they are long-lived—an IQ of 150 and a life span of 150 years—they could have more children and accumulate more wealth than the rest of us. Socially they will probably be drawn to others of their kind. With some kind of self-imposed geographical or social segregation, their genes might drift and eventually differentiate as a new species. One day, then, we will have it in our power to bring a new human species into this world. Whether we choose to follow such a path is for our descendants to decide.

**If machine efficiency became the new measure of evolutionary fitness, much of what we regard as quintessentially human would be weeded out.**



AMANA PRODUCTIONS *Getty Images (woman)*

### THE BORG ROUTE

EVEN LESS PREDICTABLE than our use of genetic manipulation is our manipulation of machines—or they of us. Is the ultimate evolution of our species one of symbiosis with machines, a human-machine synthesis? Many writers have predicted that we might link our bodies with robots or upload our minds into computers. In fact, we are already dependent on machines. As much as we build them to meet human needs, we have structured our own lives and behavior to meet theirs. As machines become ever more complex and interconnected, we will be forced to try to accommodate them. This view was starkly enunciated by George Dyson in his 1998 book *Darwin among the Machines:* "Everything that human beings are doing to make it easier to operate computer networks is at the same time, but for different reasons, making it easier for computer networks to operate human beings.... Darwinian evolution, in one of those paradoxes with which life abounds, may be a victim of its own success, unable to keep up with non-Darwinian processes that it has spawned."

Our technological prowess threatens to swamp the old ways that evolution works. Consider two different views of the future taken from an essay in 2004 by evolutionary philosopher Nick Bostrom of the University of Oxford. On the optimistic side, he wrote: "The big picture shows an overarching trend towards increasing levels of complexity, knowledge, consciousness, and coordinated goal-directed organization, a trend which, not to put too fine a point on it, we may label 'progress.' What we shall call the Panglossian view maintains that this past record of success



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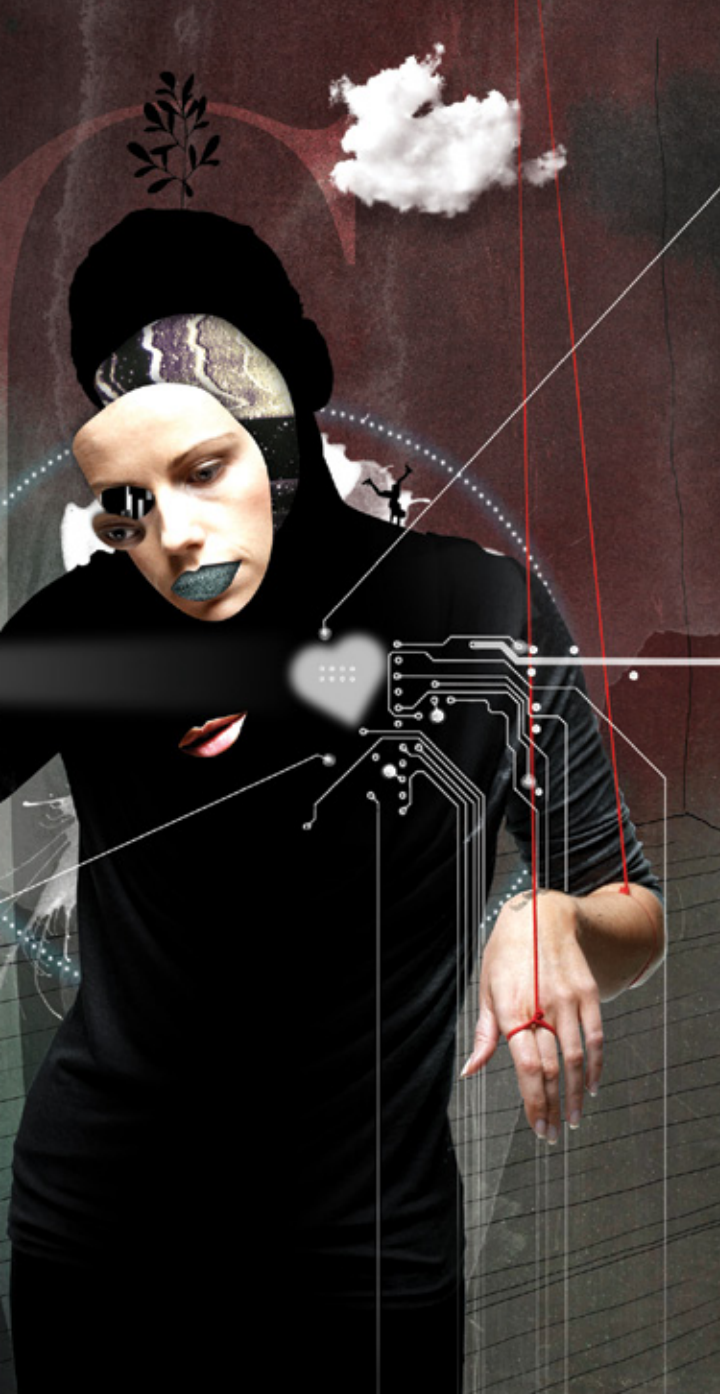

gives us good grounds for thinking that evolution (whether biological, memetic or technological) will continue to lead in desirable directions."

Although the reference to "progress" surely causes the late evolutionary biologist Steven Jay Gould to spin in his grave, the point can be made. As Gould argued, fossils, including those from our own ancestors, tell us that evolutionary change is not a continuous thing; rather it occurs in fits and starts, and it is certainly not "progressive" or directional. Organisms get smaller as well as larger. But evolution has indeed shown at least one vector: toward increasing complexity. Perhaps that is the fate of future human evolution: greater complexity through some combination of anatomy, physiology or behavior. If we continue to adapt (and undertake some deft planetary engineering), there is no genetic or evolutionary reason that we could not still be around to watch the sun die. Unlike aging, extinction does not appear to be genetically programmed into any species.

The darker side is all too familiar. Bostrom (who must be a very unsettled man) offered a vision of how uploading our brains into computers could spell our doom. Advanced artificial intelligence could encapsulate the various components of human cognition and reassemble those components into something that is no longer human—and that would render us obsolete. Bostrom predicted the following course of events: "Some human individuals upload and make many copies of themselves. Meanwhile there is gradual progress in neuroscience and artificial intelligence, and eventually it becomes possible to isolate individual cognitive modules and connect them up to modules from other uploaded minds.… Modules that conform to a common standard would be better able to communicate and cooperate with other modules and would therefore be economically more productive, creating a pressure for standardization.… There might be no niche for mental architectures of a human kind."

As if technological obsolescence were not disturbing enough, Bostrom concluded with an even more dreary possibility: if machine efficiency became the new measure of evolutionary fitness, much of what we regard as quintessentially human would be weeded out of our lineage. He wrote: "The extravagancies and fun that arguably give human life much of its meaning—humor, love, game-playing, art, sex, dancing, social conversation, philosophy, literature, scientific discovery, food and drink, friendship, parenting, sport—we have preferences and capabilities that make us engage in such activities, and these predispositions were adaptive in our species' evolutionary past; but what ground do we have for being confident that these or similar activities will continue to be adaptive in the future? Perhaps what will maximize fitness in the future will be nothing but nonstop high-intensity drudgery, work of a drab and repetitive nature, aimed at improving the eighth decimal of some economic output measure."

In short, humanity's future could take one of several routes, assuming we do not go extinct:

**Stasis.** We largely stay as we are now, with minor tweaks, mainly as races merge.

**Speciation.** A new human species evolves on either this planet or another.

**Symbiosis with machines.** Integration of machines and human brains produces a collective intelligence that may or may not retain the qualities we now recognize as human.

*Quo vadis Homo futuris?* SA

## MORE TO EXPLORE


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**Natural Selection Has Driven Population Differentiation in Modern Humans.** L. B. Barreiro, G. Laval, H. Quach, E. Patin and L. Quintana-Murci in *Nature Genetics,* Vol. 40, No. 3, pages 340–345; March 2008.

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# SCIENTIFIC AMERICAN™ Travel

# BRIGHT HORIZONS™ 17

## NORWEGIAN FJORDS, JULY 5–15, 2013

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Cruise prices vary from $2,169 for an Interior Stateroom to $7,499 for a Royal Suite, per person. For those attending our Program, there is a $1,575 fee. Port charges are $235. Government taxes and an Insight Cruises service fee are $215 per person. Gratuities are $150 per person. Program subject to change.

## Neurobiology

Speaker: Robert Sapolsky, Ph.D.

### The Biology of Memory

Consider the biology of memory. We'll start with the neurobiology of different types of memory, from the pertinent regions of the brain down to the pertinent molecules and genes. Learn about memory's impressive features, wild inaccuracies, and failings in neurological diseases. Examine individual differences in memory skills and find out how to improve your own memory capacities.

### Sushi and Middle Age

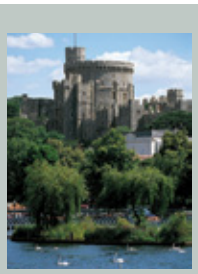
When was the last time you tried a really different, strange type of food, explored the work of a new composer, or made a substantial change in appearance? As we age, we get less interested in novelty and increasingly crave the familiar. Examine the neurobiology and psychology underlying this age-related effect.

### Humans: Are We Just Another Primate? Are We Just a Bunch of Neurons?

Dr. Sapolsky both does neurobiology research in the lab and research on wild baboons in East Africa. He'll consider human nature from these two perspectives. Are we just another primate on a continuum with all the others, or are we intrinsically special? Find out a biologist's answer.

### The Biology of Aggression and Violence

Examine the biology of violence, dealing with a single fact that makes this one of the most complicated subjects in behavioral biology — we don't hate violence, just violence in the wrong context. Looking at neurobiology, Us/Them dichotomies, hormones, evolutionary biology, and game theory, put the phenomenon of violence in a scientific context.



### Hampton Court and Windsor Castle (July 2)

Join us visiting two timeless treasures in a day designed to bring British history to life. Enhance your knowledge of Britain's history with an idyllic day trip to Windsor Castle (left) and Hampton Court Palace. They are related yet differing demonstrations of British monarchy, nationhood, and domesticity.

It's good to be Queen, and the evidence is all about you at 1,000 year old Windsor Castle. Rubens, Rembrandt, and a remarkable collection of fine art envelope you in history. Go behind the scenes at the legendary seat of the House of Windsor.

Hampton Court (also known as King Henry VIII's summer palace) is a place of royal passions and competing interests. Pomp and consequence, subterfuge and service inform the history of the palace. Our visit will put the juxtaposed Tudor and Baroque architecture, larger than life personalities, exquisite Chapel Royal, and magnificent gardens in historical context for you.

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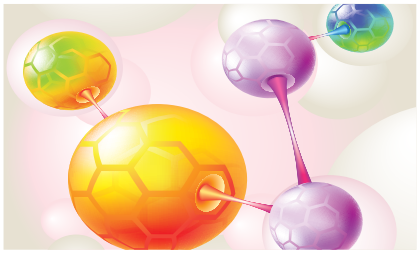


## Chemistry

Speaker: Robert Hazen, Ph.D.

### Genesis: The Scientific Quest for Life's Origins

— Is life's origin an inevitable process throughout the cosmos, or is it an improbable accident, restricted to a few planets (or only one)? How does a lifeless geochemical world of oceans, atmosphere, and rocks transform into a living planet? Find out how scientists use experimental and theoretical frameworks to deduce the origin of life.

### The Diamond Makers

Diamond forms deep in Earth when carbon experiences searing heat and crushing pressure. Decades ago General Electric scientists learned how to mimic those extreme conditions of Earth's interior in the laboratory to make synthetic diamonds. Learn the human drama and technological advances involved in producing this coveted gem and industrial tool from carbon-rich substances.

### The Story of Earth: How the Geosphere and Biosphere Co-evolved

Earth is a planet of frequent, extravagant change. Its near-surface environment has transformed over and over again across 4.5 billion years of history. Learn about the work of Dr. Hazen and colleagues that suggests that Earth's living and nonliving spheres have co-evolved over the past four billion years.

### Chemical Bonding

— The solid, liquid, and gaseous materials around us depend on the specific elements involved and the chemical bonds that hold those atoms together. By looking at the nature and significance of ionic, metallic, and covalent bonds you'll gain a new understanding of the workings of the world around you.

## Quantum Physics

Speaker: Benjamin Schumacher, Ph.D.

### Private Lives of Quantum Particles

Quantum systems can exhibit all sorts of bizarre behavior. But many of these phenomena can only be observed under conditions of the strictest privacy, where systems are "informationally isolated" from the world. These are not accidental features of quantum theory. They are inescapable facts about the microscopic world: Quantum physics is what happens when nobody is looking.

### 2π Is Not Zero (But 4π Is)

— If you rotate any geometrical shape by 360 degrees (2π radians) about any axis, you will end up with exactly the same shape. But this fact, seemingly obvious, is not true for quantum particles with spin. Learn how a rotation by 2π makes a big difference, and how it all comes down to a simple minus sign — probably the most important minus sign in all of physics. Enjoy quantum fun, demystified by Dr. Schumacher.

### The Physics of Impossible Things

Physicists find it surprising useful to ponder the impossible. Using the laws of nature, assess the possibility of science fiction's favorite phenomena and explore seemingly impossible things, which while odd, are possible. Venture into the study of impossible things and come away with an affirmation of the consistent logic of nature, and renewed wonder at real phenomena.

### The Force That Isn't a Force

— What makes a rubber band elastic? It's entropy, the microscopic disorder of its molecules. Now, entropy may provide a clue to the most familiar and mysterious of the basic forces of nature: gravity. Explore the link between entropy and gravity, and gain fascinating and unexpected insights of contemporary theoretical physics.

## Archaeology

Speaker: Kenneth Harl, Ph.D.

### From Old Europe to Roman Provinces

Explore the prehistoric foundations of Scandinavia and the Viking Age from ca. 3000 B.C. to 400 A.D. From Megalithic cultures to the arrival of Indo-Europeans, to Northern Bronze Age innovations and Celtic and Roman contributions, learn the unique environmental, cultural, and social factors that create a context for the Vikings.

### Great Halls and Market Towns in Viking Age Scandinavia

— Using archaeology and literary sources (especially saga and Eddas), learn how the "great halls" emerged as the main focus of Scandinavia civilization. Find out how the development of towns facilitated trade and were vital for the transformation and technological advance of Scandinavian society.

### Ships and Ship Building in the Viking Age

— European history records the effectiveness of the fearsome Viking longship; find out the features and technologies that made it so. Based on archaeological finds, learn about the multi-millennial evolution of the longship, from linden to oak, dugout to mast and sail. Gain an appreciation for the form and function, as well as the wider implications of Norse naval mastery for three hundred years.

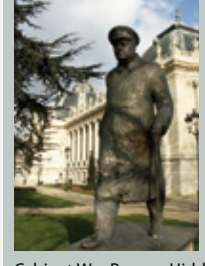
### Warfare in the Viking Age

— The Viking's applied technologies led to three centuries of robust military and economic power for Scandinavia. Discover what factors made the Vikings accomplished warriors and learn what archaeological finds tell us about Viking exploration, settlement, and development of kingdoms.

SCIENTIFIC AMERICAN Travel

# HIGHLIGHTS

**NORWEGIAN FJORDS**
**JULY 5–15, 2013**

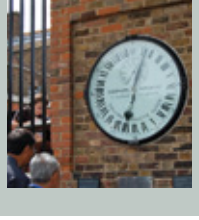


### The Royal Observatory and the Churchill War Room/Museum (July 4)

Take the road less traveled in London, visiting two less well known gems of the City, both uniquely fascinating and inspiring.

Courage, duty, shared sacrifice, and conviction are the foundation of the Churchill Cabinet War Rooms. Hidden in plain sight in the heart of London, a scant 600 miles from Berlin. Step back in time and discover how Churchill and Britain's government functioned in secrecy in these quarters, from the Blitz to VE Day. The furnishings, maps, and ephemera are as they were on VE day, May 8, 1945. Hear the stories and imagine life under bombardment in the simple and inspiring environment of the Cabinet War Rooms.

Are you the precise type? Are you a fan of Google maps or GPS? Or Cutty Sark? Join us on a tour of maritime Greenwich, where our prime objective is visiting the Royal Observatory, Greenwich, home of the Prime Meridian of the World and Greenwich Mean Time. Stroll a deeply historic corner of London significant in local, national, and international culture. See the Royal Observatory, the National Maritime Museum, the tea clipper Cutty Sark, and the Royal Naval College. Master the lingo of time — UT0, UT1, UTC, and GMT. Stand astride two hemispheres on the Prime Meridian, a moment sure to be recorded on your timeline.



### Stonehenge and Bath (July 3)

Pass a day on the Salisbury Plains and Somerset Hills, absorbing the history of two spots with ancient cultural roots.

Mute, mysterious, and megalithic, Stonehenge calls to us across the millennia. We'll respond, and walk the site in its details. Learn the significant geography, the archaeological and astronomical background, and the key stone names. But those are just the facts — the memories and true meaning of Stonehenge will be up to you.

Bath beckons the seasoned traveler. People are drawn to Bath to see its honey-colored Bath limestone buildings, and to explore its 2,000 year history as a place of relaxation and restoration. Plumb the details and nuances of Bath's fusion of architecture, culture, and history in a city with many echoes of and homages to the ancient world, while embodying the Georgian worldview.

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